

M A P P A A R L A L L										11
GTCGACCAACGGTCCGCCACGGTCCGGCCC ATG GCG CCG CCC GCC GCG CTC GCC CTC GCG CTC										66
S A A A L T L A A R P A P S P G L G P G	31									
TCC GCC GCG GCG CTC ACG CTG GCG GCC CGG CCC GCG CCT AGC CCC GGC CTC GGC CCC GGA	126									
P E C F T A N G A D Y R G T Q N W T A L	51									
CCC GAG TGT TTC ACA GCC AAT GGT GCG GAT TAT AGG GGA ACA CAG AAC TGG ACA GCA CTA	186									
Q G G K P C L F W N E T F Q H P Y N T L	71									
CAA GGC GGG AAG CCA TGT CTG TTT TGG AAC GAG ACT TTC CAG CAT CCA TAC AAC ACT CTG	246									
K Y P N G E G G L G E H N Y C R N P D G	91									
AAA TAC CCC AAC GGG GAG GGC CTG GGT GAG CAC AAC TAT TGC AGA AAT CCA GAT GGA	306									
D V S P W C Y V A E H E D G V Y W K Y C	111									
GAC GTG AGC CCC TGG TGC TAT GTG GCA GAG CAC GAG GAT GGT GTC TAC TGG AAG TAC TGT	366									
E I P A C Q M P G N L G C Y K D H G N P	131									
GAG ATA CCT GCT TGC CAG ATG CCT GGA AAC CTT GGC TGC TAC AAG GAT CAT GGA AAC CCA	426									
P P L T G T S K T S N K L T I Q T C I S	151									
CCT CCT CTA ACT GGC ACC AGT AAA ACG TCC AAC AAA CTC ACC ATA CAA ACT TGC ATC AGT	486									
F C R S Q R F K F A G M E S G Y A C F C	171									
TTT TGT CGG AGT CAG AGG TTC AAG TTT GCT GGG ATG GAG TCA GGC TAT GCT TGC TTC TGT	546									

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Fig. 1A

G	N	N	P	D	Y	W	K	Y	G	E	A	A	S	T	E	C	N	S	V	191
GGA	AAC	AAT	CCT	GAT	TAC	TGG	AAG	TAC	GGG	GAG	GCA	GCC	AGT	ACC	GAA	TGC	AAC	AGC	GTC	606
C	F	G	D	H	T	Q	P	C	G	G	D	G	R	I	I	L	F	D	T	211
TGC	TTC	GGG	GAT	CAC	ACC	CAA	CCC	TGT	GGT	GGC	GAT	GGC	AGG	ATC	ATC	CTC	TTT	GAT	ACT	666
L	V	G	A	C	G	G	N	Y	S	A	M	S	S	V	V	Y	S	P	D	231
CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	GCC	ATG	TCT	TCT	GTG	GTC	TAT	TCC	CCT	GAC	726
F	P	D	T	Y	A	T	G	R	V	C	Y	W	T	I	R	V	P	G	A	251
TTC	CCC	GAC	ACC	TAT	GCC	ACG	GGG	AGG	GTC	TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCG	GGG	GCC	786
S	H	I	H	F	S	F	P	L	F	D	I	R	D	S	A	D	M	V	E	271
TCC	CAC	ATC	CAC	TTC	AGC	TTC	CCC	CTA	TTT	GAC	ATC	AGG	GAC	TCG	GCG	GAC	ATG	GTG	GAG	846
L	L	D	G	Y	T	H	R	V	L	A	R	F	H	G	R	S	R	P	P	291
CTT	CTG	GAT	GGC	TAC	ACC	CAC	CGT	GTC	CTA	GCC	CGC	TTC	CAC	GGG	AGG	AGC	CGC	CCA	CCT	906
L	S	F	N	V	S	L	D	F	V	I	L	Y	F	F	S	D	R	I	N	311
CTG	TCC	TTC	AAC	GTC	TCT	CTG	GAC	TTC	GTC	ATC	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	966
Q	A	Q	G	F	A	V	L	Y	Q	A	V	K	E	E	L	P	Q	E	R	331
CAG	GCC	CAG	GGA	TTT	GCT	GTT	TTA	TAC	CAA	GCC	GTC	AAG	GAA	GAA	CTG	CCA	CAG	GAG	AGG	1026

Fig. 1B

P A V N Q T V A E V I T E Q A N L S V S	351
CCC GCT GTC AAC CAG ACG GTG GCC GAG GTG ATC ACG GAG CAG GCC AAC CTC AGT GTC AGC	1086
A A R S S K V L Y V I T T S P S H P P Q	371
GCT GCC CGG TCC TCC AAA GTC CTC TAT GTC ATC ACC ACC AGC CCC AGC CAC CCA CCT CAG	1146
T V P G S N S W A P P M G A G S H R V E	391
ACT GTC CCA GGT AGC AAT TCC TGG GCG CCA CCC ATG GGG GCT GGA AGC CAC AGA GTT GAA	1206
G W T V Y G L A T L L I L T V T A I V A	411
GGA TGG ACA GTC TAT GGT CTG GCA ACT CTC CTC ATC ACA GTC ACA GCC ATT GTA GCA	1266
K I L L H V T F K S H R V P A S G D L R	431
AAG ATA CTT CTG CAC GTC ACA TTC AAA TCC CAT CGT GTT CCT GCT TCA GGG GAC CTT AGG	1326
D C H Q P G T S G E I W S I F Y K P S T	451
GAT TGT CAT CAA CCA GGG ACT TCG GGG GAA ATC TGG AGC ATT TTT TAC AAG CCT TCC ACT	1386
S I S I F K K K L K G Q S Q Q D D R N P	471
TCA ATT TCC ATC TTT AAG AAG AAA CTC AAG GGT CAG AGT CAA CAA GAT GAC CGC AAT CCC	1446
L V S D *	476
CTT GTG AGT GAC TAA	1461

Fig. 1C

AAACCCACTGTGCCCTAGGACTTGGAGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGTTCTTCTC 1540  
TGACAGACTCTTCCCTCTCCTCTCCTCTGCGCTTTCGGGAAACCCTCCTCTACAGACTAGGAAGAGGCACCT 1620  
GCTGCCAGGGCAGGACAGCTGGATTCTCCTGCTT 1657

**Fig. 1D**

GTCGACCCACGGTCCGCCCGGCTCCCGGTGCTGCCCCCTCTGCCCCGGCGCGCGGGGTCCCGCACTGACGGCC 79  
  
M A P P A A R L A L L S A A A L T L A 19  
C ATG GCG CCG CCC GCC GCC CGT CTC GCG CTG CTC TCC GCC GCT GCG CTC ACT CTG GCG 137  
  
A R P A P G P R S G P E C F T A N G A D 39  
GCC CGG CCC GCG CCC GGT CCC CGC TCC GGC CCC GAG TGC TTC ACA GCC AAC GGT GCA GAT 197  
  
Y R G T Q S W T A L Q G G K P C L F W N 59  
TAC AGG GGA ACA CAG AGC TGG ACA GCG CTG CAA GGT GGG AAG CCA TGT CTG TTC TGG AAC 257  
  
E T F Q H P Y N T L K Y P N G E G L G 79  
GAG ACT TTC CAG CAT CCG TAC AAC ACG CTG AAG TAC CCC AAC GGG GAA GGA GGA CTG GGC 317  
  
E H N Y C R N P D G D V S P W C Y V A E 99  
GAG CAC AAT TAT TGC AGA AAT CCA GAT GGA GAC GTG AGC CCT TGG TGC TAC GTG GCC GAG 377

**Fig.1E**

H	E	D	G	V	Y	W	K	Y	C	E	I	P	A	C	Q	M	P	G	N	119
CAT	GAG	GAC	GGA	GTC	TAC	TGG	AAG	TAC	TGT	GAA	ATT	CCT	GCC	TGC	CAG	ATG	CCT	GGA	AAC	437
L	G	C	Y	K	D	H	G	N	P	P	P	L	T	G	T	S	K	T	S	139
CTT	GGC	TGC	TAC	AAG	GAT	CAT	GGA	AAC	CCA	CCT	CCT	CTC	ACG	GGC	ACC	AGT	AAA	ACC	TCT	497
N	K	L	T	I	Q	T	C	I	S	F	C	R	S	Q	R	F	K	F	A	159
AAC	AAG	CTC	ACC	ATA	CAA	ACC	TGT	ATC	AGC	TTC	TGT	CGG	AGT	CAG	AGA	TTC	AAG	TTT	GCT	557
G	M	E	S	G	Y	A	C	F	C	G	N	N	P	D	Y	W	K	H	G	179
GGG	ATG	GAG	TCA	GGC	TAT	GCC	TGC	TTC	TGT	GGG	AAC	AAT	CCT	GAC	TAC	TGG	AAG	CAC	GGG	617
E	A	A	S	T	E	C	N	S	V	C	F	G	D	H	T	Q	P	C	G	199
GAG	GCG	GCC	AGC	ACC	GAG	TGC	AAT	AGT	GTC	TGC	TTC	GGG	GAC	CAC	ACG	CAG	CCC	TGC	GGT	677
G	D	G	R	I	I	L	F	D	T	L	V	G	A	C	G	G	N	Y	S	219
GGG	GAC	GGC	AGG	ATT	ATC	CTC	TTT	GAC	ACT	CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	737
A	M	A	A	V	V	Y	S	P	D	F	P	D	T	Y	A	T	G	R	V	239
GCC	ATG	GCA	GCC	GTG	GTG	TAC	TCC	CCT	GAC	TTC	CCT	GAC	ACC	TAC	GCC	ACT	GGC	AGA	GTC	797
C	Y	W	T	I	R	V	P	G	A	S	R	I	H	F	N	F	T	L	F	259
TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCA	GGA	GCC	TCT	CGC	ATC	CAT	TTC	AAC	TTC	ACC	CTG	TTT	857
D	I	R	D	S	A	D	M	V	E	L	L	D	G	Y	T	H	R	V	L	279
GAT	ATC	AGG	GAC	TCT	GCA	GAC	ATG	GTG	GAG	CTG	CTG	GAC	GGC	TAC	ACC	CAC	CGC	GTC	CTG	917

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Fig.1F

V	R	L	S	G	R	S	R	P	P	L	S	F	N	V	S	L	D	F	V	299
GTC	CGG	CTC	AGT	GGG	AGG	AGC	CGC	CCG	CCT	CTG	TCT	TTC	AAT	GTC	TCT	CTG	GAT	TTT	GTC	977
I	L	Y	F	F	S	D	R	I	N	Q	A	Q	G	F	A	V	L	Y	Q	319
ATT	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	CAG	GCC	CAG	GGA	TTT	GCT	GTG	TTG	TAC	CAA	1037
A	T	K	E	E	P	P	Q	E	R	P	A	V	N	Q	T	L	A	E	V	339
GCC	ACC	AAG	GAG	GAA	CCG	CCA	CAG	GAG	AGA	CCT	GCT	GTC	AAC	CAG	ACC	CTG	GCA	GAG	GTG	1097
I	T	E	Q	A	N	L	S	V	S	A	A	H	S	S	K	V	L	Y	V	359
ATC	ACC	GAG	CAA	GCC	AAC	CTC	AGT	GTC	AGC	GCT	GCC	CAC	TCC	TCC	AAA	GTC	CTC	TAT	GTC	1157
I	T	P	S	P	S	H	P	P	Q	T	A	Q	V	A	I	P	G	H	R	379
ATC	ACC	CCC	AGC	CCC	AGC	CAC	CCT	CCG	CAG	ACT	GCC	CAG	GTA	GCC	ATT	CCT	GGG	CAC	CGT	1217
Q	L	G	P	T	A	T	E	W	K	D	G	L	C	T	A	W	R	P	S	399
CAG	TTG	GGG	CCA	ACA	GCC	ACA	GAG	TGG	AAG	GAT	GGA	CTG	TGT	ACG	GCC	TGG	CGA	CCC	TCC	1277
S	S	S	Q	S	Q	Q	L	S	Q	R	F	F	C	M	S	H	L	N	L	419
TCA	TCC	TCA	CAG	TCA	CAG	CAG	TTG	TCG	CAA	AGA	TTC	TTC	TGC	ATG	TCA	CAT	TTA	AAT	CTC	1337
I	E	S	L	H	Q	E	T	L	G	T	V	V	S	L	G	L	L	E	I	439
ATC	GAG	TCC	CTG	CAT	CAG	GAG	ACC	TTA	GGG	ACT	GTC	GTC	AGC	CTG	GGG	CTT	CTG	GAG	ATA	1397
S	G	P	F	S	M	N	L	P	L	Q	S	P	S	L	R	R	S	S	R	459
TCT	GGA	CCA	TTT	TCT	ATG	AAC	CTT	CCA	CTA	CAA	TCT	CCA	TCT	TTA	AGA	AGA	AGC	TCA	AGG	1457

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Fig.1G

V	R	V	N	K	M	T	A	I	P	S	*	
GTC	AGA	GTC	AAC	AAG	ATG	ACC	GCA	ATC	CCC	TCG	TGA	1493
GTG	ACT	GAAG	CCCC	CAC	GCC	CTG	CAT	GAG	AGG	CTCC	GCTCG	AGTTT
CTG	CCCT	TCCC	ATT	CAC	CA	CTCT	TTT	GG	AG	CA	CCCT	GGAT
GTAC	AGCC	TGCT	GCT	CTG	CTGG	GATG	GTAA	GA	CA	AGCC	AGGCT	GACAG
CTCT	TGGG	TGGT	GGG	AGG	TAT	AGT	GTAG	GAT	GAG	TTT	CTCT	CTCT
CCCT	GTCT	TTAC	AGTT	TG	CAAT	AG	AGCC	AG	ACT	GAA	GA	CTGTC
GTGG	CAATT	GGCC	CTAG	AGCC	CCAG	AGT	GTAG	GC	TTT	CTG	CTG	CCCA
AGTCC	GAGG	GA	CTG	AG	CA	CCAG	ATGT	CA	TTT	CTAG	AGG	TTCT
GGCA	AGCC	TG	AGG	ATT	GT	CCAT	GG	AA	CTG	GA	ACT	TTCT
TAGC	CTCA	AGT	AGT	AGT	AGT	AGT	AGT	AGT	AGT	AGT	AGT	AGT
AGCT	GGG	CTG	TAG	CTG	GGG	CTG	TAG	CTG	GGG	CTG	TAG	CTG
TGGG	CTG	TAG	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA
GGCT	GTAG	CC	TAG	CTG	GGG	CTG	TAG	CTG	GGG	CTG	TAG	CTG
GACCC	TAGG	TTCT	ATCC	AG	CA	CTAT	CA	GA	AGG	TGG	AG	AA
TTCT	ACGT	GAG	GTG	TCAT	CA	TTT	AA	AG	CA	GA	TCAT	CA
AGAG	TAGG	AGT	AAGG	CTCT	GT	CT	CA	TT	GT	CT	CA	TT
GATCC	TCC	AG	AA	AG	CTG	CA	AG	AT	TG	CA	AG	AT
CTG	AGT	CTG	GGA	AGT	GG	CTG	CA	AG	AT	TG	CA	AG
GCCT	CTG	CTC	TGG	TACC	CT	CT	GG	AA	CA	CT	CT	CT
TCCT	CTAG	CTG	CTC	CC	AG	ACT	GT	GG	GA	TC	AG	AG
TGAC	CTG	AGT	CA	CC	AG	AG	CA	CA	AG	AG	AG	AG
TAC	AGG	G	TACT	AA	GT	CA	TT	GA	TC	TT	GA	TC
CACT	ACAT	AA	GA	AC	CA	CT	GA	AG	CA	CT	GA	AG

Fig.1H

CCCTGAGACCAAGTGTGAGTCACAGAGTGCCATGTGCGTAGTGCCATAAAGGATATGGGTTCTTAACCAGGGAAGGCTC 3310  
 ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACCTCACCTGTCTCTTCCT 3389  
 ATCTCGGACACAGGAAGCAAGCCCCAGTGTGGTGCGAGCTGCGGCTCAGCATTTGGTGTCCCCAGGAAGGCGGTGGATG 3468  
 TGGCCACGCTCCTTTTGCTGTGGCCCTGGCACAGCCCCAACACTGCAGGGCCCCACCTTCTCTCTTGGGGGTAGGGACAC 3547  
 ATAAGGAAACCTAACCCACCTCCAAACACAGCAGAGGACAGTGGGAAGGAGGCTGTAAATCACCCAGGCCAGACCTC 3626  
 CAGAAATGACAGGCACAGTCTGTTAGAACCTGTAGGCAGCCAGTCACAGAGGGCCTTTGTGCTGGTAACACCCCTGCCTG 3705  
 GAGCATAGGGGTAAGCCGAGGAGAGAGCAGCCCTCAGAGACATCAGCTAAAACATAGGTGCCCTATGTCCCTCCCT 3784  
 TCCTGTCACTGCTTACAAAGCAGAGACAGAGTAGGAAAAGGTCTTCATCCTCTCCCACATCAGCAAGGATAGGGCT 3863  
 GCGGCTGCCCTAAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGCTCTGGCTTCAGACTCCTCAGCCA 3942  
 AAAGCTCTTGAAGATCAAAAGCTCTGGCGGTACAGCTGTCTGGCCTGTGGCCAGCCCATGGGATGTGCTGGCCAG 4021  
 GTGCCACCCACGGCTCACTGTCAATCCAGGAGGACCCACCTGATGCTCCTCATCATCCGCTGGCTGACACTATCA 4100  
 GAGCTCGCGCCGGCTGTTGCCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGATGGCCTCCAGA 4179  
 CTCTGTACGCCCTCTGCAGGGCCACACAAGTCTCCGAGCCAAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCCT 4258  
 GTGGAGTGTCCCTGTTGATGTCTGAGGTCTGCTTTGGGTACCGCCCTGGGAACCTGCTAACCTCCGATTGGTCCCTTGT 4337  
 GTCTCTGTTTACTGTCCTCTTCTACCTCCAGGTCACTTAGCTCTGGCTGCTCTGGCTGGGAGTGGGGGTGGGATGCT 4416  
 GGCTGACCCCCACCTGGTCTGCCAACAGAACCTGGGGCCCTCACACGGGCTCCTGTCTTGCCAAAGCTGGAGCTGAGC 4495  
 ACACTGGCCAGGCTGAGTGGGCAGAGCAACAAGTGGAAGGGATCTCTCCTTAGAGGGAGGTGGCCGAAGGTGT 4574  
 AGATCCAGCGAGGAGTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAAATCTCACCCCTCCAGCAG 4653  
 GGATATGACTTTGGACAACAAGGCTTTATTTGTAATAATGCTCTTAATATGCAACTTTGAGAAATAAGATAGAAACATCA 4732  
 TGTATTTTAAATATAAAATGAAGTGTGACACACTGTATACAATTTAATATATATTTTAGGATTTTGTATTAAAGAA 4811  
 AATGGAATGTGATGGTACTTAACTTTTACAAAAGAGAGAAAATGTTATTTTACTGTTTGAAGAAAATAAATATTCTCA 4890  
 TTGTTGTAGAAAAAATAAAAAAAGGGCGGCGCGC 4928

Fig.11



	10	20	30	40	50	60	70
Hum.	MAPPAARLALLSAAALTLAARPA	SPGLGP	CEFTANGADYRGTQNW	TALQGGKPC	CLFWNETFQHPYNT		
	.....	.....	.....	.....	.....	.....	.....
Mur.	MAPPAARLALLSAAALTLAARPA	PGPR--SGPECFTANGADYRGTQSW	TALQGGKPC	CLFWNETFQHPYNT			

	80	90	100	110	120	130	140
Hum.	LKYPNGEGGLGEHNYCRNPDG	VDSPWCYVAEHEDGVYWKYCEI	PACQMPGNLGCYKD	HGNPPPLTGTSKT			
	.....	.....	.....	.....	.....	.....	.....
Mur.	LKYPNGEGGLGEHNYCRNPDG	VDSPWCYVAEHEDGVYWKYCEI	PACQMPGNLGCYKD	HGNPPPLTGTSKT			
	70	80	90	100	110	120	130

	150	160	170	180	190	200	210
Hum.	SNKLT	IQTCISFCRSQR	FKFAGMESGYAC	FCGNNPDYWKYGEAA	STECNSVCFGDHTQ	PCGGDGRIILFD	
	.....	.....	.....	.....	.....	.....	.....
Mur.	SNKLT	IQTCISFCRSQR	FKFAGMESGYAC	FCGNNPDYWKHGEAA	STECNSVCFGDHTQ	PCGGDGRIILFD	
	140	150	160	170	180	190	200

	220	230	240	250	260	270	280
Hum.	TLVGACGGNYSAMSSVVYSPDFDTYATGRVCYWTIRVPGASHIHFSFPLFDIRSADMVELLDGYTHRV						
	::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::						
Mur.	TLVGACGGNYSAMAAVVYSPDFDTYATGRVCYWTIRVPGASRIHFNFTLFDIRSADMVELLDGYTHRV						
	210	220	230	240	250	260	270

	290	300	310	320	330	340	350
Hum.	LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVILYQAVKEELPQERPAVNQTVAEVITEQANLSV						
	:..	:..	:..	:..	:..	:..	:..
Mur.	LVRLSGRSRPPPLSFNVSLDFVILYFFSDRINQAQGFVILYQATKEEPPQERPAVNQTVAEVITEQANLSV						
	280	290	300	310	320	330	340
	360	370	380	390	400	410	420
Hum.	SAARSSKVLYVITTSPPSHPPQTVPGSNSWAPPMGAGSHRVEGWTVYGLATLLILTVTAIVAKILLHVTFK						
	:..	:..	:..	:..	:..	:..	:..
Mur.	SAAHSSKVLYVITTSPPSHPPQTAQVAIPGHRQLGPTA---TEWKD-GLCTAWRPSSSSQSQQLSQRFFCM						
	350	360	370	380	390	400	410
	430	440	450	460	470		
Hum.	SHRVPASGDLRDCHQPGTSGEIWSIFYKPPSTISIFKKKLGQSQ-QDDRNPLVSD						
	::	::	::	::	::	::	::
Mur.	SHLNLIESHQETLGTGVVSLGLLEISGPFMSNPLPLQSPSLRRSSRVVKNKMTAIPS						
	420	430	440	450	460	470	

Fig.1K

004250" 09084560

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Fig. 1L

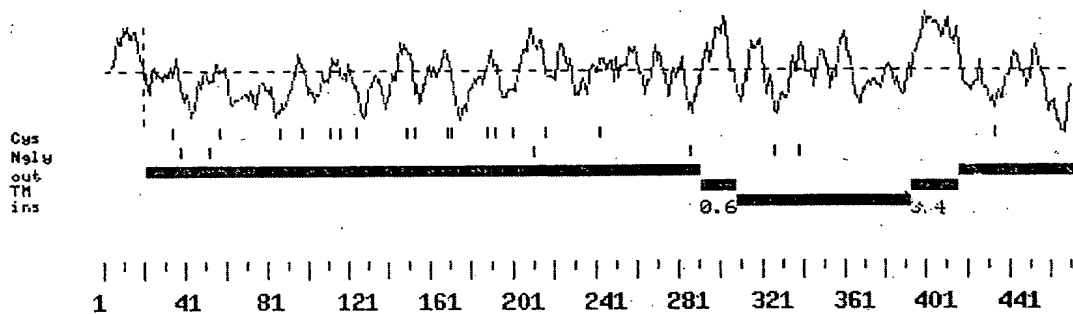
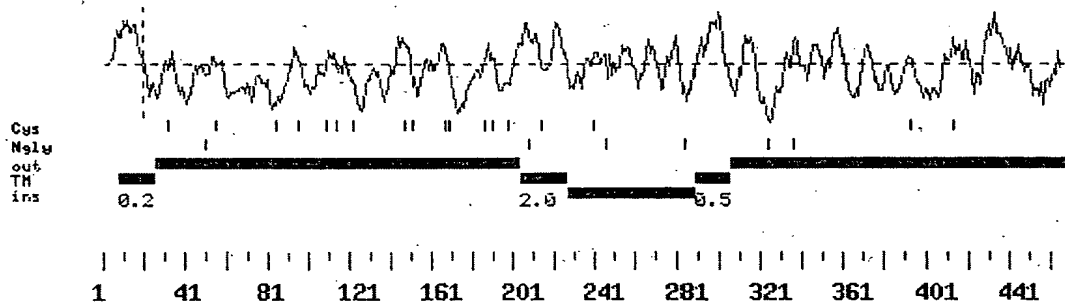


Fig. 1M



GCGGCCGCTCGGATCTAGAACTAGTA	M	M	L	P	Q	N	S	W	H	I	D	F	G	13
ATG ATG CTG CCT CAA AAC TCG TGG CAT ATT GAT TTT GGA														66
R C C C H Q N L F S A V T C I L L L N														33
AGA TGC TGC TGT CAT CAG AAC CTT TTC TCT GCT GGT GTC GTC ATC CTG CTC CTG AAT														126
S C F L I S S F N G T D L E L R L V N G														53
TCC TGC TTT CTC ATC AGC AGT TTT AAT GGA ACA GAT TTG GAG TTG AGG CTG GTC AAT GGA														186
D G P C S G T V E V K F Q G Q W G T V C														73
GAC GGT CCC TGC TCT GGG ACA GTG GAG GTG AAA TTC CAG GGA CAG TGG GGG ACT GTG TGT														246
D D G W N T T A S T V V C K Q L G C P F														93
GAT GAT GGG TGG AAC ACT ACT GCC TCA ACT GTC GTG TGC AAA CAG CTT GGA TGT CCA TTT														306
S F A M F R F G Q A V T R H G K I W L D														113
TCT TTC GCC ATG TTT CGT TTT GGA CAA GCC GTG ACT AGA CAT GGA AAA ATT TGG CTT GAT														366
D V S C Y G N E S A L W E C Q H R E W G														133
GAT GTT TCC TGT TAT GGA AAT GAG TCA GCT CTC TGG GAA TGT CAA CAC CGG GAA TGG GGA														426
S H N C Y H G E D V G V N C Y G E A N L														153
AGC CAT AAC TGT TAT CAT GGA GAA GAT GTT GGT GTG AAC TGT TAT GGT GAA GCC AAT CTG														486

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Fig. 2A

G	L	R	L	V	D	G	N	N	S	C	S	G	R	V	E	V	K	F	Q	173
GGT	TTG	AGG	CTA	GTG	GAT	GGA	AAC	AAC	TCC	TGT	TCA	GGG	AGA	GTG	GAG	GTG	AAA	TTC	CAA	546
E	R	W	G	T	I	C	D	D	G	W	N	L	N	T	A	A	V	V	C	193
GAA	AGG	TGG	GGG	ACT	ATA	TGT	GAT	GAT	GGG	TGG	AAC	TTG	AAT	ACT	GCT	GCC	GTG	GTG	TGC	606
R	Q	L	G	C	P	S	S	F	I	S	S	G	V	V	N	S	P	A	V	213
AGG	CAA	CTA	GGA	TGT	CCA	TCT	TCT	TTT	ATT	TCT	TCT	GGA	GTT	GTT	AAT	AGC	CCT	GCT	GTA	666
L	R	P	I	W	L	D	D	I	L	C	Q	G	N	E	L	A	L	W	N	233
TTG	CGC	CCC	ATT	TGG	CTG	GAT	GAC	ATT	TTA	TGC	CAG	GGG	AAT	GAG	TTG	GCA	CTC	TGG	AAT	726
C	R	H	R	G	W	G	N	H	D	C	S	H	N	E	D	V	T	L	T	253
TGC	AGA	CAT	CGT	GGA	TGG	GGA	AAT	CAT	GAC	TGC	AGT	CAC	AAT	GAG	GAT	GTC	ACA	TTA	ACT	786
C	Y	D	S	S	D	L	E	L	R	L	V	G	G	T	N	R	C	M	G	273
TGT	TAT	GAT	AGT	AGT	GAT	CTT	GAA	CTA	AGG	CTT	GTA	GGT	GGA	ACT	AAC	CGC	TGT	ATG	GGG	846
R	V	E	L	K	I	Q	G	R	W	G	T	V	C	H	H	K	W	N	N	293
AGA	GTA	GAG	CTG	AAA	ATC	CAA	GGA	AGG	TGG	GGG	ACC	GTA	TGC	CAC	CAT	AAG	TGG	AAC	AAT	906
A	A	A	D	V	V	C	K	Q	L	G	C	G	T	A	L	H	F	A	G	313
GCT	GCA	GCT	GAT	GTC	GTA	TGC	AAG	CAG	TTG	GGA	TGT	GGA	ACC	GCA	CTT	CAC	TTC	GCT	GGC	966
L	P	H	L	Q	S	G	S	D	V	V	W	L	D	G	V	S	C	S	G	333
TTG	CCT	CAT	TTG	CAG	TCA	GGG	TCT	GAT	GTT	GTA	TGG	CTT	GAT	GGT	GTC	TCC	TGC	TCC	GGT	1026

Fig. 2B

N E S F L W D C R H S G T V N F D C L H	353
AAT GAA TCT TTT CTT TGG GAC TGC AGA CAT TCC GGA ACC GTC AAT TTT GAC TGT CTT CAT	1086
Q N D V S V I C S D G A D L E L R L A D	373
CAA AAC GAT GTG TCT TGT ATC TGC TCA GAT GGA GCA GAT TTG GAA CTG CGA CTA GCA GAT	1146
G S N N C S G R V E V R I H E Q W T I	393
GGA AGT AAC AAT TGT TCA GGG AGA GTA GAG GTG AGA ATT CAT GAA CAG TGG TGG ACA ATA	1206
C D Q N W K N E Q A L V V C K Q L G C P	413
TGT GAC CAG AAC TGG AAG AAT GAA CAA GCC CTT GTG GTT TGT AAG CAG CTA GGA TGT CCG	1266
F S V F G S R R A K P S N E A R D I W I	433
TTC AGC GTC TTT GGC AGT CGT CGT GCT AAA CCT AGT AAT GAA GCT AGA GAC ATT TGG ATA	1326
N S I S C T G N E S A L W D C T Y D G K	453
AAC AGC ATA TCT TGC ACT GGG AAT GAG TCA GCT CTC TGG GAC TGC ACA TAT GAT GGA AAA	1386
A K R T C F R R S D A G V I C S D K A D	473
GCA AAG CGA ACA TGC TTC CGA AGA TCA GAT GCT GGA GTA ATT TGT TCT GAT AAG GCA GAT	1446
L D L R L V G A H S P C Y G R L E V K Y	493
CTG GAC CTA AGG CTT GTC GGG GCT CAT AGC CCC TGT TAT GGG AGA TTG GAG GTG AAA TAC	1506
Q G E W G T V C H D R W S T R N A V V	513
CAA GGA GAG TGG GGG ACT GTG TGT CAT GAC AGA TGG AGC ACA AGG AAT GCA GCT GTT GTG	1566

Fig. 2C

C	K	Q	L	G	C	G	K	P	M	H	V	F	G	M	T	Y	F	K	E	533
TGT	AAA	CAA	TTG	GGA	TGT	GGA	AAG	CCT	ATG	CAT	GTG	TTT	GGT	ATG	ACC	TAT	TTT	AAA	GAA	1626
A	S	G	P	I	W	L	D	D	V	S	C	I	G	N	E	S	N	I	W	553
GCA	TCA	GGA	CCT	ATT	TGG	CTG	GAT	GAC	GTT	TCT	TGC	ATT	GGA	AAT	GAG	TCA	AAT	ATC	TGG	1686
D	C	E	H	S	G	W	G	K	H	N	C	V	H	R	E	D	V	I	V	573
GAC	TGT	GAA	CAC	AGT	GGA	TGG	GGA	AAG	CAT	AAT	TGT	GTA	CAC	AGA	GAG	GAT	GTG	ATT	GTA	1746
T	C	S	G	D	A	T	W	G	L	R	L	V	G	G	S	N	R	C	S	593
ACC	TGC	TCA	GGT	GAT	GCA	ACA	TGG	GGC	CTG	AGG	CTG	GTG	GGC	GGC	AGC	AAC	CGC	TGC	TCG	1806
G	R	L	E	V	Y	F	Q	G	R	W	G	T	V	C	D	D	G	W	N	613
GGA	AGA	CTG	GAG	GTG	TAC	TTT	CAA	GGA	CGG	TGG	GGC	ACA	GTG	TGT	GAT	GAC	GGC	TGG	AAC	1866
S	K	A	A	A	V	V	C	S	Q	L	D	C	P	S	S	I	I	G	M	633
AGT	AAA	GCT	GCA	GCT	GTG	GTG	TGT	AGC	CAG	CTG	GAC	TGC	CCA	TCT	TCT	ATC	ATT	GGC	ATG	1926
G	L	G	N	A	S	T	G	Y	G	K	I	W	L	D	D	V	S	C	D	653
GGT	CTG	GGA	AAC	GCT	TCT	ACA	GGA	TAT	GGA	AAA	ATT	TGG	CTC	GAT	GAT	GTT	TCC	TGT	GAT	1986
G	D	E	S	D	L	W	S	C	R	N	S	G	W	G	N	N	D	C	S	673
GGA	GAT	GAG	TCA	GAT	CTC	TGG	TCA	TGC	AGG	AAC	AGT	GGG	TGG	GGA	AAT	AAT	GAC	TGC	AGT	2046
H	S	E	D	V	G	V	I	C	S	D	A	S	D	M	E	L	R	L	V	693
CAC	AGT	GAA	GAT	GTT	GGA	GTG	ATC	TGT	TCT	GAT	GCA	TCG	GAT	ATG	GAG	CTG	AGG	CTT	GTG	2106

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Fig. 2D

G	G	S	S	R	C	A	G	K	V	E	V	N	V	Q	G	A	V	G	I	713
GGT	GGA	AGC	AGC	AGG	TGT	GCT	GGA	AAA	GTT	GAG	GTG	AAT	GTC	CAG	GGT	GCC	GTG	GGA	ATT	2166
L	C	A	N	G	W	G	M	N	I	A	E	V	V	C	R	Q	L	E	C	733
CTG	TGT	GCT	AAT	GGC	TGG	GGA	ATG	AAC	ATT	GCT	GAA	GTT	GTT	TGC	AGG	CAA	CTT	GAA	TGT	2226
G	S	A	I	R	V	S	R	E	P	H	F	T	E	R	T	L	H	I	L	753
GGG	TCT	GCA	ATC	AGG	GTC	TCC	AGA	GAG	CCT	CAT	TTC	ACA	GAA	AGA	ACA	TTA	CAC	ATC	TTA	2286
M	S	N	S	G	C	T	G	G	E	A	S	L	W	D	C	I	R	W	E	773
ATG	TCG	AAT	TCT	GGC	TGC	ACT	GGA	GGG	GAA	GCC	TCT	CTC	TGG	GAT	TGT	ATA	CGA	TGG	GAG	2346
W	K	Q	T	A	C	H	L	N	M	E	A	S	L	I	C	S	A	H	R	793
TGG	AAA	CAG	ACT	GCG	TGT	CAT	TTA	AAT	ATG	GAA	GCA	AGT	TTG	ATC	TGC	TCA	GCC	CAC	AGG	2406
Q	P	R	L	V	G	A	D	M	P	C	S	G	R	V	E	V	K	H	A	813
CAG	CCC	AGG	CTG	GTT	GGA	GCT	GAT	ATG	CCC	TGC	TCT	GGA	CGT	GTT	GAA	GTG	AAA	CAT	GCA	2466
D	T	W	R	S	V	C	D	S	D	F	S	L	H	A	A	N	V	L	C	833
GAC	ACA	TGG	CGC	TCT	GTC	TGT	GAT	TCT	GAT	TTC	TCT	CTT	CAT	GCT	GCC	AAT	GTG	CTG	TGC	2526
R	E	L	N	C	G	D	A	I	S	L	S	V	G	D	H	F	G	K	G	853
AGA	GAA	TTA	AAT	TGT	GGA	GAT	GCC	ATA	TCT	CTT	TCT	GTG	GGA	GAT	CAC	TTT	GGA	AAA	GGG	2586
N	G	L	T	W	A	E	K	F	Q	C	E	G	S	E	T	H	L	A	L	873
AAT	GGT	CTA	ACT	TGG	GCC	GAA	AAG	TTC	CAG	TGT	GAA	GGG	AGT	GAA	ACT	CAC	CTT	GCA	TTA	2646

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Fig. 2E



C	P	I	V	Q	H	P	E	D	T	C	I	H	S	R	E	V	G	V	V	893
TGC	CCC	ATT	GTT	CAA	CAT	CCG	GAA	GAC	ACT	TGT	ATC	CAC	AGC	AGA	GAA	GTT	GGA	GTT	GTC	2706
C	S	R	Y	T	D	V	R	L	V	N	G	K	S	Q	C	D	G	Q	V	913
TGT	TCC	CGA	TAT	ACA	GAT	GTC	CGA	CTT	GTG	AAT	GGC	AAA	TCC	CAG	TGT	GAC	GGG	CAA	GTG	2766
E	I	N	V	L	G	H	W	G	S	L	C	D	T	H	W	D	P	E	D	933
GAG	ATC	AAC	GTG	CTT	GGA	CAC	TGG	GGC	TCA	CTG	TGT	GAC	ACC	CAC	TGG	GAC	CCA	GAA	GAT	2826
A	R	V	L	C	R	Q	L	S	C	G	T	A	L	S	T	T	G	G	K	953
GCC	CGT	GTT	CTA	TGC	AGA	CAG	CTC	AGC	TGT	GGG	ACT	GCT	CTC	TCA	ACC	ACA	GGA	GGA	AAA	2886
Y	I	G	E	R	S	V	R	V	W	G	H	R	F	H	C	L	G	N	E	973
TAT	ATT	GGA	GAA	AGA	AGT	GTT	CGT	GTG	TGG	GGA	CAC	AGG	TTT	CAT	TGC	TTA	GGG	AAT	GAG	2946
S	L	L	D	N	C	Q	M	T	V	L	G	A	P	P	C	I	H	G	N	993
TCA	CTT	CTG	GAT	AAC	TGT	CAA	ATG	ACA	GTT	CTT	GGA	GCA	CCT	CCC	TGT	ATC	CAT	GGA	AAT	3006
T	V	S	V	I	C	T	G	S	L	T	Q	P	L	F	P	C	L	A	N	1013
ACT	GTC	TCT	GTG	ATC	TGC	ACA	GGA	AGC	CTG	ACC	CAG	CCA	CTG	TTT	CCA	TGC	CTC	GCA	AAT	3066
V	S	D	P	Y	L	S	A	V	P	E	G	S	A	L	I	C	L	E	D	1033
GTA	TCT	GAC	CCA	TAT	TTG	TCT	GCA	GTT	CCA	GAG	GGC	AGT	GCT	TTG	ATC	TGC	TTA	GAG	GAC	3126
K	R	L	R	L	V	D	G	D	S	R	C	A	G	R	V	E	I	Y	H	1053
AAA	CGG	CTC	CGC	CTA	GTG	GAT	GGG	GAC	AGC	CGC	TGT	GCC	GGG	AGA	GTA	GAG	ATC	TAT	CAC	3186

Fig. 2F

D	G	F	W	G	T	I	C	D	D	G	W	D	L	S	D	A	H	V	V	1073
GAC	GGC	TTC	TGG	GGC	ACC	ATC	TGT	GAT	GAC	GGC	TGG	GAC	CTG	AGC	GAT	GCC	CAC	GTG	GTG	3246
C	Q	K	L	G	C	G	V	A	F	N	A	T	V	S	A	H	F	G	E	1093
TGT	CAA	AAG	CTG	GGC	TGT	GGA	GTG	GCC	TTC	AAT	GCC	ACG	GTC	TCT	GCT	CAC	TTT	GGG	GAG	3306
G	S	G	P	I	W	L	D	D	L	N	C	T	G	T	E	S	H	L	W	1113
GGG	TCA	GGG	CCC	ATC	TGG	CTG	GAT	GAC	CTG	AAC	TGC	ACA	GGA	ACG	GAG	TCC	CAC	TTG	TGG	3366
Q	C	P	S	R	G	W	G	Q	H	D	C	R	H	K	E	D	A	G	V	1133
CAG	TGC	CCT	TCC	CGC	GGC	TGG	GGG	CAG	CAC	CAC	TGC	AGG	CAC	AAG	GAG	GAC	GCA	GGG	GTC	3426
I	C	S	E	F	T	A	L	R	L	Y	S	E	T	E	T	E	S	C	A	1153
ATC	TGC	TCA	GAA	TTC	ACA	GCC	TTG	AGG	CTC	TAC	AGT	GAA	ACT	GAA	ACA	GAG	AGC	TGT	GCT	3486
G	R	L	E	V	F	Y	N	G	T	W	G	S	V	G	R	R	N	I	T	1173
GGG	AGA	TTG	GAA	GTC	TTC	TAT	AAC	GGG	ACC	TGG	GGC	AGC	GTC	GGC	AGG	AGG	AAC	ATC	ACC	3546
T	A	I	A	G	I	V	C	R	Q	L	G	C	G	E	N	G	V	V	S	1193
ACA	GCC	ATA	GCA	GGC	ATT	GTG	TGC	AGG	CAG	CTG	GGC	TGT	GGG	GAG	AAT	GGA	GTT	GTC	AGC	3606
L	A	P	L	S	K	T	G	S	G	F	M	W	V	D	D	I	Q	C	P	1213
CTC	GCC	CCT	TTA	TCT	AAG	ACA	GGC	TCT	GGT	TTC	ATG	TGG	GTG	GAT	GAC	ATT	CAG	TGT	CCT	3666
K	T	H	I	S	I	W	Q	C	L	S	A	P	W	E	R	R	I	S	S	1233
AAA	ACG	CAT	ATC	TCC	ATA	TGG	CAG	TGC	CTG	TCT	GCC	CCA	TGG	GAG	CGA	AGA	ATC	TCC	AGC	3726

Fig. 2G

P	A	E	E	T	W	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTG	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086
N	A	S	S	G	H	L	A	L	I	L	S	S	I	F	G	L	L	L	L	1373
AAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206
R	V	S	T	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	T	1413
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAT	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266

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Fig. 2H

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C	L	K	R	E	D	P	H	G	T	R	T	S	D	D	T	P	N	H	G	1433
TGC	CTC	AAG	AGA	GAG	GAC	CCA	CAT	GGG	ACA	AGA	ACC	TCA	GAT	GAC	ACC	CCC	AAC	CAT	GGT	4326

C	E	D	A	S	D	T	S	L	L	G	V	L	P	A	S	E	A	T	K
TGT	GAA	GAT	GCT	AGC	GAC	ACA	TCG	CTG	TTG	GGA	GTT	CTT	CCT	GCC	TCT	GAA	GCC	ACA	AAA

★	1454
TGA	4389

CTTTAGACTTCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAGGAGACAACAACCTTTAAATGAATAAAGAGGA 4468  
AGTCAAGTTGCCCTATGGAAAACCTGTCCAATAACATTTCTTGAACAAATAGGAGAACAGCTAAATTGATAAAGACTGG 4547  
TGATAATAAAAAATTGAATTATGTATATCACTGTTAAAAAATAAAAAAATAAAAAAACAACGGACCGTGGGTGG 4626  
AC 4628

**Fig. 21**

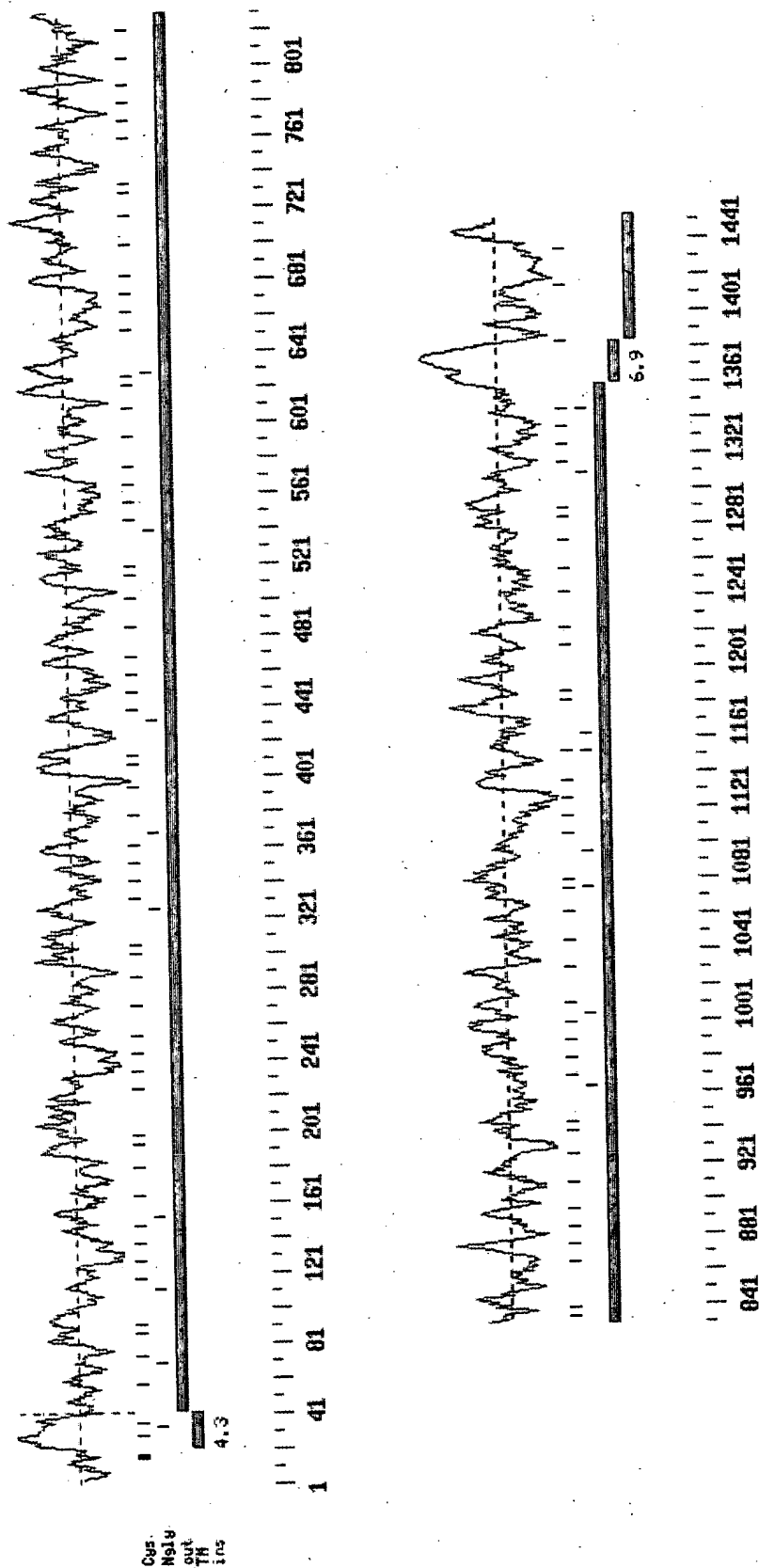


Fig. 2J

Hum.	10	20	30	40	50	60	70
	MMLPQNSWHIDFGRCCCHQNLFS	AVVTCILLNSCFLISSFN	GTDLRLVNGDGPCSGT	VEVKFQGWG			
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	10	20	30	40	50		
	MAL-----GR---	HLSRLGL---	CVLLLT---	MVG---	GQALELRLKDG	VHRCEGRVEVKHQGEWG	
Hum.	80	90	100	110	120	130	
	TVCDDGWN	TTASTVVCKQLGCPFS	FAMRFGQAVTR-HGKI	WDDVSCYGNESALWECQ	---	REWGSHN	
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	60	70	80	90	100	110	
	TVDGYRWT	LKDA	SVVCRQLGCGAAIG-F	PGGAYFG	PLGLPIWLLY	TSCEGT	ESTVSDCEHSNIKDYRNDG
Hum.	140	150	160	170	180	190	200
	CYHG	EDVGVN	CYGEANLGLRLVD	GNNSCSGRVEVKFQ	ERWGTICDDGWN	LNTAAV	VCRQLGCPSSFISG
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	120	130	140	150	160	170	180
	YNHGRD	AGVVC	SG----FVRL	AGDGPCSGRVEVH	SGEAWIPVSDGN	FTLATAQI	ICAE
Hum.	210	220	230	240	250	260	270
	VVNSPA	VL	PIW	DDILCQ	GNELALWNC	RHRGWNHDCSHNED	VTLT
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
WC1	190	200	210	220	230	240	250
	HEL	FRESSAQV	WAAEF	FRCEGE	EPELW	VCPRVPCPGGTCH	HSGSAQVVC

Fig. 2K

Hum.	280	290	300	310	320	330	340	
	LKIQRWGT	CHHKWNA	ADVCKQL	CGGTAL	HFAGLPH	LQSGSD	VVWL	DGVSCSGNESFLWDCRHS
	...	...	...	...	...	...	...	...
WC1	MNISQWRAL	CASHWSLAN	ANVICRQL	CGGVAIST	PGPHLVEE	GDIILTAR	FHC	SGAESFLWSCPVTAL
	260	270	280	290	300	310	320	
Hum.	350	360	370	380	390	400	410	
	VNFDCLHQ	NDVSVIC	SDGADLE	RLRLADG	SNCSGR	VEVRHEQ	WWTICD	QNWKNEQALVCKQLGCPFSV
	.	...	...	...	...	...	...	...
WC1	GGPDCSH	GNTASVICS	-GNQI	-----	QVLPQCND	-----	SV	
	330	340			350			
Hum.	420	430	440	450	460	470	480	
	FGSRRAK	PSNEARDI	WINSISCT	GNESAL	WDCTYD	GKAKRTC	FRRSDAG	VICSDKADLRLVGAHSPCY
	...	...	...	...	...	...	...	...
WC1	-----	SQPTGSA	-----	ASEDSA	-----	PY	-----	CSDSRQL--RLVDGGGPCA
	360				370		380	
Hum.	490	500	510	520	530	540	550	
	GRLEVKY	QGEWGT	VCHDRW	STRNA	AAVVC	KLGC	KPMHV	FGMTYFKEASGPIWLDDVSCIGNESNIWDCE
	...	...	...	...	...	...	...	...
WC1	GRVEILD	QGSWGT	ICDDG	WDLDD	ARVVC	RQLGCC	EALNAT	GSAHFGAGSGPIWLDNLNCTGKESHVWRCP
	390	400	410	420	430	440	450	

Fig. 2L





840	850	860	870	880	890	900
Hum.	NCGDAISLSVGDHFGKGNGLTWA	KFKQCEGSETHALALCP	IVQHPEDTCIHSRE	VGVCSRYTDVRLV-NG		
	:: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::
WC1	GCGKAVSVLGHMPFRES	DGQVAAEFRC	DGGEPELWSC	PRVPCPGGTC	LSHSGAAQVVC	SVYTEVQLMKNG
	740	750	760	770	780	790 800
910	920	930	940	950	960	970
Hum.	KSQCDGQVEINVLGH	WGLCDTHWD	PEDARVLC	RQLSCGTALSTTG	GKYIGERSVR	VWGRFHC
	:: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::
WC1	TSQCEGQVEMKISGR	WRALCASHWSLANAN	VVCRQLGCGVA	ISTPRGPHL	VEGGDQISTAQ	FHC
	810	820	830	840	850	860 870
980	990	1000	1010	1020	1030	1040
Hum.	LDNCQMTVLGAPPC	IHGNTVSVICTG	SLTQPLFPCLAN	VSDPYLSAVPEGS	ALICLEDKRLRL	VDDGDSRC
	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::
WC1	LWSCPVTALGGPDC	SHGNTASVICS	GNHTQVLPQC	NDFLSQ	PAGSAASEESS	PYCSDSRQLRLV
	880	890	900	910	920	930 940
1050	1060	1070	1080	1090	1100	1110
Hum.	AGRVEIYH	DGFWGTICDD	GWDLSDAH	VVCQKLGCG	VAFNATVSAHF	GEGSGPIWLDDL
	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::	: :: ::::
WC1	GGRVEILD	QGSWGTICDD	DDARVVC	RQLGCC	EALNATGSAHF	GAGSGPIWLDDL
	950	960	970	980	990	1000 1010

Fig. 2N

```

1120      1130      1140      1150      1160      1170      1180
Hum. PSRGWQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLG
      :::::::::::::::::::: : : :::::::::::::::::::: : : ::::::::::::::::::::
WC1 PSRGWGRHDCRHKEDAGVICSEFLALRMVSEDQQ--CAGWLEVFYNGTWGSVCRSPMEDITTVSVICRQLG
      1020      1030      1040      1050      1060      1070

1190      1200      1210      1220      1230      1240
Hum. CGENGVVSLAPLSKTGSGFMWVDDIQCPKTHISIWQCLSA PWERRISSPAEETWITCEDR-----
      ::::: . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 CGDSGSLNTSVGLREGSRPRWVDLIQCRKMDTSLWQCPSPWKYSSCSPKEEAYISCEGRRPKSCPTAAA
1080      1090      1100      1110      1120      1130      1140

1250      1260      1270      1280      1290      1300
Hum. -----IRVRGGDTECSGRVEIWHAGSWGTVCDSDWDLAEAEVVCQQLGCGSALALRDASFQGTGTIW
      .:::::::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : :
WC1 CTDREKLRLRGDSECSGRVEVWHNGSWGTVCDSDWSLAEAEVVCQQLGCGQALEAVRSAAFPGNGSIW
1150      1160      1170      1180      1190      1200      1210

1310      1320      1330      1340      1350      1360
Hum. LDDMRCKGNEFLWDCHAKPWGQSDCGHKEDAGVRCG-----QSLKSLNASSGHLALI
      ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 LDEVQCGGRESSLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLPTTTAGTRTTSNSLPGFISLPGLCLI
1220      1230      1240      1250      1260      1270      1280

```

Fig. 20

	1370	1380	1390	1400	1410
Hum.	LSSIFGLLLVLFI	LTWCRVQK-----	QKHLPLRV	S-----	TRRRG-----SLEENLFHEME
	: : : :	: : : :	:	: : :	: : : :
WC1	LGSLLFLVLVI	VTQLLRW-RAERRAL	SSYEDALAEAVYEELDY	LLTQKEGLGSPDQM	TDVPDENYDDAE
1290	1300	1310	1320	1330	1340 1350
		1420	1430		1440
Hum.	TC-----	LKREDPHGTRTSD-----	DTPNHGCEDAS-----		DTSLLG
	.	: : : : .	. . . . :	:	: : :
WC1	EVPVPGTPSPSQGN	EEVPEKEDGVRSSQTGS	FLNFSREAA	NPGEGEESFWLLQ	GKGAGYDDVELSA
1360	1370	1380	1390	1400	1410 1420
	1450				
Hum.	LPASEAT-K				
	:	: : :			
WC1	LGTSPTVS				
	1430				

**Fig. 2P**



Fig. 20iii

	560	570	580	590	600	610	620
Hum.	ACTTGAATACTGCTGCCGTGCTGTCAGGCAACTAGGATGTCCTCTTTTATTCTTCTGGAGTTGT						
	...	...	...	...	...	...	...
WC1	TCACACTTGCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG						
	490	500			510		520
	630	640	650	660	670	680	690
Hum.	TAATAGCCCTGCTGTATTGCGCCCCATTGGCTGGATGACATTTTATGCCAGGGGAATGAGTTGGCACT-						
	...	...	...	...	...	...	...
WC1	TTGTGGC-----AAGGCTG--TGTCTGT-----CCTGGGACATGAG-----CTCTT						
	530		540		550		560
	700	710	720	730	740	750	760
Hum.	CTGGAATTGCAGACATCGTGGATGGGGAATCATGACTGCAGTCACAATGAGGATGTCACATTAAC TTGT						
	...	...	...	...	...	...	...
WC1	CAGAGAGTCCAGT-GCC-----CAGGCTG--GGC-----TGAAGAGTTCA-----GG						
	570	580		590		600	
	770	780	790	800	810	820	830
Hum.	TATGATAGTAGTATCTTGAACCTAAGGCTTGTAGGTGGAACCTAACCGCTGTATGGGAGAGTAGAGCTGA						
	...	...	...	...	...	...	...
WC1	TGTGAGGGGAGGAGCCTGAGCT-----CT-----GGGTCTGCCC-CAGAGTG-----CCCTG-						
	610	620	630		640		650

Fig. 2Qiii

	840	850	860	870	880	890	900
Hum.	AAATCCAAGGAGTGGGGACCGTATGCCACCATAAGTGAACAATGCTGCAGCTGATGTCGTATGCAA						
	840	850	860	870	880	890	900
WC1	-----TCCA-----GGGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT						
	660	670	680	690	700		
	910	920	930	940	950	960	970
Hum.	GCAGTTGGGATGTGGAACCGCACTTCACCTTCGCTGGCTTGCCCTCATTTCAGCTCAGGGTCTGATGTTGTA						
	910	920	930	940	950	960	970
WC1	-----CAGAAAGTCCGGCTCATGACAA-AC-GGCT--CCTC-TCAG-TGTGAAGGGCAGGTGGAGAT						
	710	720	730	740	750	760	
	980	990	1000	1010	1020	1030	1040
Hum.	TGGCTTGATGGTGTCTCCTGCTCCGGTAATGAATCTTTCTTTGGACTGCAGACATTCCGGAACCGTCA						
	980	990	1000	1010	1020	1030	1040
WC1	-----TCTG-GACAATGGAGAGCGCTCTGTGCCTCCC-ACTGGAGTCTGGCCAATGCC---A						
	770	780	790	800	810	820	
	1050	1060	1070	1080	1090	1100	1110
Hum.	ATTTTGACTGTCTTCATCAAAACGATGTGTCTGTGATCTGTCTCAGATGGAGCAGATTGGAACTGCGACT						
	1050	1060	1070	1080	1090	1100	1110
WC1	ATGTTATCTGTCGTCAGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAG-----GACCAC-ACT						
	830	840	850	860	870	880	

Fig. 2Qiv





Fig. 2Qvi

1670	1680	1690	1700	1710	1720	1730
Hum.	ACACAGTGGATGGGAAAGCATAATTGTGTACACAGAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA					
.	:	:	:	:	:	:
1370	1380	1390	1400	1410	1420	1430
WC1	TTCCCGGGCTGGGGCAGCACAACTGCAGACACAAGCAGGACGCGGGTCACTCTGCTCAG--AGTTC-					
1740	1750	1760	1770	1780	1790	1800
Hum.	ACATGGGGCCCTGAGGCTGGTGGCGGCAGCAACCGCTGCTCGGAAGACTGGAGGTGTACTTTCAAGGAC					
.	:	:	:	:	:	:
1440	1450	1460	1470	1480	1490	1500
WC1	-CT--GGCCCTCAGGATGGTGAGTGAGGACCAGCAGTGCTGCTGGGTGGCTGGAAGTTTCTACAATGGGA					
1810	1820	1830	1840	1850	1860	1870
Hum.	GGTGGGCACAGTGTGTGATGACGGCTGGAACAGTAAGCTGCAGCTGTGGTGTAGCCAGCTGGACTG					
.	:	:	:	:	:	:
1510	1520	1530	1540	1550	1560	1570
WC1	CCTGGGCAGTGTCTGCCGTAACCCCATGGAAGACATCACTGTGTCCACGATCTGCAGACAGCTTGGCTG					
1880	1890	1900	1910	1920	1930	1940
Hum.	CCCATCTTCTATCATTTGGCATGGGTCTG-GGAAACGCTTCTA-CAGGATATGGAAAAATTTGGCTCGATG					
.	:	:	:	:	:	:
1580	1590	1600	1610	1620	1630	
WC1	T--GGGGACAGTGGAAACCCTCAACTCTTCTGTGTCTTTAGAGAAGGTTTTAGGCCACAGTGGGTGGAT-					

**Fig. 2Qvii**

	1950	1960	1970	1980	1990	2000	2010
Hum.	ATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGTG--GGGAAATAATGAC						
	.....	.....	.....	.....	.....	.....	.....
WC1	-AGATCCAGTGTCCGAAACTGACACCTCTCT---CTGGCAGTGTCCCTCTGACCCCTTGAATTACAAC						
	1640	1650	1660	1670	1680	1690	1700
	2020	2030	2040	2050	2060	2070	2080
Hum.	TGCAGTCACAGTGAAGATGTTGGAGTG-ATCTGTTCTGATG-CATCGGATATGAGCTGAGGCTGTGGG						
	:: ::	.....	:: ::	.....	:: ::	:: ::	.....
WC1	T-CATGCTCTCCAAGGAGGAAGCCTATATCTGTTGTGCAGACAGCAGACA--GATCCGC--CTGGTGGA						
	1710	1720	1730	1740	1750	1760	
	2090	2100	2110	2120	2130	2140	2150
Hum.	TGAAGCAGCAGGTGTGCTGGAAGTTGAGGTGAATGTCCAGGGTCCCGTGGGAATTCTGTGTGCTAAT						
	.....	:: ::	.....	.....	.....	.....	.....
WC1	TGGAGGTGGTCGCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGCACCATCTGTGATGAC						
	1770	1780	1790	1800	1810	1820	1830
	2160	2170	2180	2190	2200	2210	2220
Hum.	GGCTGGGGAATGAACATTGCTGAAGTTGTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCA						
	.....	.....	.....	.....	.....	.....	.....
WC1	CGCTGGGACCTGGACGATGCCCGTGTGTTGTGCAAGCAGCTGGGCTGTGGAGAAGC---CCTGGACGCCA						
	1840	1850	1860	1870	1880	1890	1900

Fig. 2Qviii

**Fig. 2Qix**



	2780	2790	2800	2810	2820	2830	2840
Hum.	TGTGTGACACCCACTGGGACCAGAAAGATGCCCGTGTCTCTATGCAGACAGCTCAGCTGTGGACTGCTCT						
	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :						
WC1	TCTGTGCCCTCCCACCTGGAGTCTGGCCAATGCCAATGTTGTCTGTCTGTCAGCTCGGCTGTGGAGTCGCCCAT						
	2460	2470	2480	2490	2500	2510	2520
	2850	2860	2870	2880	2890	2900	2910
Hum.	CTCAACCACAGGAGGAAAAATATATTGGAGAAAGAAGTGTTCGTGTGGGACACAGGTTTCATTGCTTA						
	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :						
WC1	CTCCACCCCCAGAGACCACACTTGGTGGAAGGAGGTGATCAGATCTCAACAGCCCCAATTTCACTGCTCA						
	2530	2540	2550	2560	2570	2580	2590
	2920	2930	2940	2950	2960	2970	2980
Hum.	GGGAATGAGTCACCTTCTGGATAACTGTCAAATGACAGTTCTTGGAGCACCTCCCTGTATCCATGGAAATA						
	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :						
WC1	GGGGCTGAGTCCTTCCTGTGGAGTTGTCTGTGACTGCCTTGGTGGCCTGACTGTTCCTCATGGCAACA						
	2600	2610	2620	2630	2640	2650	2660
	2990	3000	3010	3020	3030	3040	3050
Hum.	CTGTCTCTGTGATCTGCACAGGAAGCCTGACCCAGCCACTGTTCCATGCCCTCGCAATGTATCTGACCC						
	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : ~:						
WC1	CAGCCTCTGTGATCTGCTCAGGAAACCCACACCCAGGTGCTGCCCCAGTGCAACGACTTCCTGTCTCAACC						
	2670	2680	2690	2700	2710	2720	2730

**Fig. 2Qxi**

	3060	3070	3080	3090	3100	3110	3120
Hum.	ATATTGCTGCAGTTC	CAGAGGGCAGTGCTTT	GATCTGCTTAGAGGACA	AAACGGCTCCGCCTAGTGGAT			
	.	.....	.....	.....	.....	.....	.....
WC1	TGCAGGCTCTGCGGCCT	CAGAGGAGAGTTCTCC	TACTGCTCAGACAGCAG	CGCTCCGCCTGGTGGAC			
	2740	2750	2760	2770	2780	2790	2800
	3130	3140	3150	3160	3170	3180	3190
Hum.	GGGACAGCCGCTGTGCC	GGGAGAGTAGAGATCT	ATCACGACGGCTTCTGG	GGCACCATCTGTGATGACG			
	.....	.....	.....	.....	.....	.....	.....
WC1	GGGGCGGTCCCTGCGG	CGGAGAGTGGAGATCCT	TGACCAAGGCTCCTGG	GCACCATCTGTGATGATG			
	2810	2820	2830	2840	2850	2860	2870
	3200	3210	3220	3230	3240	3250	3260
Hum.	GCTGGACCTGAGCGATG	CCCCACGTGGTGTGTCA	AAAGCTGGGCTGTGGAG	TGGCCTTCAATGCCACGGT			
	.....	.....	.....	.....	.....	.....	.....
WC1	ACTGGGACCTGGACGAT	GCCCCGTGTGGTGTGC	AGGCAGCTGGGCTGTGG	AGAAGCCCTCAATGCCACGGG			
	2880	2890	2900	2910	2920	2930	2940
	3270	3280	3290	3300	3310	3320	3330
Hum.	CTCTGCTCACTTGGGG	AGGGTCAAGGCCCATCT	GGCTGGATGACCTGAAC	TGCACAGGAACGGAGTCC			
	.....	.....	.....	.....	.....	.....	.....
WC1	GTCTGCTCACTTCGGG	GCAGGATCAGGGCCCAT	CTGGCTGGACGACCTGA	ACTGCACAGGAAGGAGTCC			
	2950	2960	2970	2980	2990	3000	3010

Fig. 2Qxiii

```

3340      3350      3360      3370      3380      3390      3400
Hum.  CACTTGTGGCAGTGCCCTTCCCGCGGCTGGGGGCAGCACGACTGCAGGCACAAGGAGGACGCAGGGGTCA
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  CACGTGTGGAGGTGCCCTTCCCGGGCTGGGGCGGCACGACTGCAGACACAAGGAGGACGCCGGGGTCA
3020      3030      3040      3050      3060      3070      3080

3410      3420      3430      3440      3450      3460      3470
Hum.  TCTGCTCAGAATTACAGCCCTTGAGGCTCTACAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGA
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  TCTGCTCAGAGTTCCTGGCCCTCAGGAT----GGTGAG-CGAGGACCAGCAG-TGTGCTGGGTGGCTGGA
3090      3100      3110      3120      3130      3140

3480      3490      3500      3510      3520      3530      3540
Hum.  AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACACAGCCATAGCAGGCATTGTG
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  GGTTTCTACAACGGGACCTGGGGCAGTGTCTGCCGCAGCCCCCATGGAAGATATCACTGTGTCCCGTGATC
3150      3160      3170      3180      3190      3200      3210

3550      3560      3570      3580      3590      3600
Hum.  TGCAGGCAGCTGGGCTGTGGGAGAATGGAGTTGTACAGCCTCGCCCCCTTA--TCT-AAGACAGGCTCTG
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  TGCAGACAGCTTGGATGTGGGGACAGTGGA--AGTCT-CAACACCTCTGTGTGCTCTCAGGGAAGGTTCTA
3220      3230      3240      3250      3260      3270      3280

```

Fig. 2Q<sup>iii</sup>



```

3610      3620      3630      3640      3650      3660      3670
Hum. GTTTCATGTGGGTGGATGACATTCAAGTGTCTAAACGCATATCTCCATATGGCAGTGCCTGTCTGCCCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 GACCCCGGTGGTAGATTAAATTCAGTGTCTCGGAAATGGATACCTCTCTCTGGCAGTGTCTTCTGCCCC
3290      3300      3310      3320      3330      3340      3350

3680      3690      3700      3710      3720      3730      3740
Hum. ATGGGAGCGAAGAAATCTCCAGCCCAGCAGAGACCTGGATCACATGTGAAGATAGAATA---AGAG-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 ATGGAAATACAGTTCATGTCTCTCCAAAGGAGGAGCCTACATCTCATGTGAAGGAAGACCCCAAGAGC
3360      3370      3380      3390      3400      3410      3420

Hum. -----TGC-----GTGGAGGAGACACCGAGTGTCTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 TGTCCAACTGTGCGCCTGCACAGACAGAGAGAAGCTCCGCCTCAGGGGAGGAGACAGCGAGTGTCTCAG
3430      3440      3450      3460      3470      3480      3490

3770      3780      3790      3800      3810      3820      3830
Hum. GGAGAGTGGAGATCTGGCAGCAGGCTCTGGGCACAGTGTGTGATGACTCCTGGGACCTGGCCGAGGC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1 GCGGGGTGGAGGTGTGGCACAACGGCTCTCTGGGCACCGTGTGCGATGACTCCTGGAGCCTGGCAGAGGC
3500      3510      3520      3530      3540      3550      3560

```

Fig. 2Qxiv

```

3840      3850      3860      3870      3880      3890      3900
Hum.  GGAAGTGTGTGTCAGCAGCTGGGCTGTGGCTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTTGGCCAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  TGAGTGTGTGTCAGCAGCTGGGCTGTGGCCAGGCCCTGGAAGCCGCTGCGGTCTGCAGCATTTGGCCCT
3570      3580      3590      3600      3610      3620      3630

3910      3920      3930      3940      3950      3960      3970
Hum.  GGAAGTGAACCATCTGGTTGGATGACATGCGGTGCAAGGAAATGAGTCATTCTATGGGACTGTCACG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  GGAATGGGAGCATCTGGCTGGACGAGGTGCAGTGCAGTGGGGCGGAGTCCTCCCTGTGGACTGTGTG
3640      3650      3660      3670      3680      3690      3700

3980      3990      4000      4010      4020      4030      4040
Hum.  CCAAACTGGGGACAGAGTGACTGTGGACACAAAGGAAGATGCTGGCGTGAGGTGCTCTGG---ACAGTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  CGAGCCCTGGGGCAGAGCGACTGCAAGCACGAGGAGGATGCTGGTGTGAGGTGCTCTGGTGTAAAGGAC
3710      3720      3730      3740      3750      3760      3770

4050      4060      4070      4080      4090
Hum.  G-----CTGAAATCACTGAATG--CCT-----CCTCAGGT-CATT---TAGCA-CTTATTTATCCA
      : . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1  AACATTGCCCCACGACCACAGCAGGGACAGAACCAACCTCAAATTCTCTCCCTGGCATCTTCTCCCTGCCT
3780      3790      3800      3810      3820      3830      3840

```

Fig. 2Qxv

```

4100      4110      4120      4130      4140
Hum. G-----TATCTT---TGGGCTC-CTTCTC---CTGGTTCT-----GTTTATTCTATTCTCA
:      :      :      :      :      :      :      :      :      :      :
WC1 GGGGTTCTCTGCCTTATCCTGGGTCGCTTCTCTTCCCTGGTCCCTCGTCACTCCTGGTCACTCAGCTACTCA
3850      3860      3870      3880      3890      3900      3910

4150      4160      4170      4180
Hum. CGTGGTG--CCGAGTTCAGAAACAAAAACATCT-----GCCC---CT---CAGAGTTT-----
:      :      :      :      :      :      :      :      :      :      :
WC1 GATGGAGACAGAGCGCAGAGCCCTTATCCAGCTATGAAGATGCTCTTGCTGAAGCTGTGTATGAGGAGCT
3920      3930      3940      3950      3960      3970      3980

4190      4200      4210      4220
Hum. -----CAAC-----CAGAAAGGAGGG---GTTCT-CTCG---AGGAGAAATTATCCATGA-----
:      :      :      :      :      :      :      :      :      :      :
WC1 CGATTACCTTCTGACACAGAAAGGAAGGTCTGGGCAGCCCAGATCAGATGACTGATGTCCCCTGATGAAAAAT
3990      4000      4010      4020      4030      4040      4050

4230      4240      4250
Hum. ---GATGGAG-----ACCTG-----CCTC-----AAGAGAGAGGAC
:      :      :      :      :      :      :      :      :      :      :
WC1 TATGATGATGCTGAAGAAGTACCAGTGCCTGGAACCTCCTTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC
4060      4070      4080      4090      4100      4110      4120

```

Fig. 2Qxvi

```

4260      4270      4280      4290
Hum. CCACATGGGACAAGAAC-----CTCAGA-TGACAC---CC-----CCAA-----
      :: :: :::: ::::: ::::: ::::: ::::: ::::: :::::
WC1  CCCCAGAGAAGGAGGACGGGTGAGGTCCTCTCAGACAGGCTCTTTCCCTGAAC TTCTCCAGAGGCAGC
4130      4140      4150      4160      4170      4180      4190

      4300      4310      4320      4330
Hum. ----CCATGGTT--GTGAAGA----TGCTAGCGACAC-----ATCGCTG--TTGGGAGTT
      :: :: . ::::: : ::::: ::::: .. ::::: . . :::::
WC1  TAATCCTGGGAAGGAGAAGAGAGCTTCTGGCTGCTCCAGGGGAAGAAAGGGGATGCTGGGTATGATGAT
4200      4210      4220      4230      4240      4250      4260

      4340      4350
Hum. CTT-----CCTG-----CCTCTGAAGCCACAAA
      :: :::: ::::: ::::: ::::: . . .
WC1  GTTGAAC TCAGTCCCCTGGGAACATCCCCAGTGACTTTCTCTCG
4270      4280      4290      4300

```

Fig. 2Qxvii

GTCGACCCACGCGTCCGGTCTGTGGCTGAGC	ATG	GCC	CTC	CCA	GCC	CTG	GGC	CTG	GAC	CCC	TGG	AGC	12
													67
L L G L F L F L Q L L Q L L L L P T T A G													32
CTC CTG GGC CTT TTC CTC TTC CAA CTG CTT CAG CTG CTG CCG ACG ACG ACC GCG GGG													127
G G G Q G P M P R V R Y Y A G D E R A													52
GGA GGC GGC CAG GGC CCC ATG CCC AGG GTC AGA TAC TAT GCA GGG GAT GAA CGT AGG GCA													187
L S F F H Q K G L Q D F D T L L L S G D													72
CTT AGC TTC TTC CAC CAG AAG GGC CTC CAG GAT TTT GAC ACT CTG CTC CTG AGT GGT GAT													247
G N T L L Y V G A R E A I L A L D I Q D P													92
GGA AAT ACT CTC TAC GTG GGG GCT CGA GAA GCC ATT CTG GCC TTG GAT ATC CAG GAT CCA													307
G V P R L K N M I P W P A S D R K K S E													112
GGG GTC CCC AGG CTA AAG AAC ATG ATA CCG TGG CCA GCC AGT GAC AGA AAA AAG AGT GAA													367
C A F K K K S N E T Q C F N F I R V L V													132
TGT GCC TTT AAG AAG AAG AGC AAT GAG ACA CAG TGT TTC AAC TTC ATC CGT GTC CTG GTT													427
S Y N V T H L Y T C G T F A F S P A C T													152
TCT TAC AAT GTC ACC CAT CTC TAC ACC TGC GGC ACC TTC GCC TTC AGC CCT GCT TGT ACC													487
F I E L Q D S Y L L P I S E D K V M E G													172
TTC ATT GAA CTT CAA GAT TCC TAC CTG TTG CCC ATC TCG GAG GAC AAG GTC ATG GAG GGA													547

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Fig. 3A

K	G	Q	S	P	F	D	P	A	H	K	H	T	A	V	L	V	D	G	M	192
AAA	GGC	CAA	AGC	CCC	TTT	GAC	CCC	GCT	CAC	AAG	CAT	ACG	GCT	GTC	TTG	GTG	GAT	GGG	ATG	607
L	Y	S	G	T	M	N	N	F	L	G	S	E	P	I	L	M	R	T	L	212
CTC	TAT	TCT	GGT	ACT	ATG	AAC	AAC	TTC	CTG	GGC	AGT	GAG	CCC	ATC	CTG	ATG	CGC	ACA	CTG	667
G	S	Q	P	V	L	K	T	D	N	F	L	R	W	L	H	H	D	A	S	232
GGA	TCC	CAG	CCT	GTC	CTC	AAG	ACC	GAC	AAC	TTC	CTC	CGC	TGG	CTG	CAT	CAT	GAC	GCC	TCC	727
F	V	A	A	I	P	S	T	Q	V	V	Y	F	F	F	E	E	T	A	S	252
TTT	GTG	GCA	GCC	ATC	CCT	TCG	ACC	CAG	GTC	GTC	TAC	TTC	TTC	TTC	GAG	GAG	ACA	GCC	AGC	787
E	F	D	F	F	E	R	L	H	T	S	R	V	A	R	V	C	K	N	D	272
GAG	TTT	GAC	TTC	TTT	GAG	AGG	CTC	CAC	ACA	TCG	CGG	GTG	GCT	AGA	GTC	TGC	AAG	AAT	GAC	847
V	G	G	E	K	L	L	Q	K	K	W	T	T	F	L	K	A	Q	L	L	292
GTG	GGC	GGC	GAA	AAG	CTG	CTG	CAG	AAG	AAG	TGG	ACC	ACC	TTC	CTG	AAG	GCC	CAG	CTG	CTC	907
C	T	Q	P	G	Q	L	P	F	N	V	I	R	H	A	V	L	L	P	A	312
TGC	ACC	CAG	CCG	GGG	CAG	CTG	CCC	TTC	AAC	GTC	ATC	CGC	CAC	GCG	GTC	CTG	CTC	CCC	GCC	967
D	S	P	T	A	P	H	I	Y	A	V	F	T	S	Q	W	Q	V	G	G	332
GAT	TCT	CCC	ACA	GCT	CCC	CAC	ATC	TAC	GCA	GTC	TTC	ACC	TCC	CAG	TGG	CAG	GTT	GGC	GGG	1027
T	R	S	S	A	V	C	A	F	S	L	L	D	I	E	R	V	F	K	G	352
ACC	AGG	AGC	TCT	GCG	GTT	TGT	GCC	TTC	TCT	TCT	CTC	TTG	GAC	ATT	GAA	CGT	GTC	TTT	AAG	1087

Fig. 3B

K	Y	K	E	L	N	K	E	T	S	R	W	T	T	Y	R	G	P	E	T	372
AAA	TAC	AAA	GAG	TTG	AAC	AAA	GAA	ACT	TCA	CGC	TGG	ACT	ACT	TAT	AGG	GGC	CCT	GAG	ACC	1147
N	P	R	P	G	S	C	S	V	G	P	S	S	D	K	A	L	T	F	M	392
AAC	CCC	CGG	CCA	GGC	AGT	TGC	TCA	GTG	GGC	CCC	TCC	TCT	GAT	AAG	GCC	CTG	ACC	TTC	ATG	1207
K	D	H	F	L	M	D	E	Q	V	V	G	T	P	L	L	V	K	S	G	412
AAG	GAC	CAT	TTC	CTG	ATG	GAT	GAG	CAA	GTG	GTG	GGG	ACG	CCC	CTG	CTG	GTG	AAA	TCT	GGC	1267
V	E	Y	T	R	L	A	V	E	T	A	Q	G	L	D	G	H	S	H	L	432
GTG	GAG	TAT	ACA	CGG	CTT	GCA	GTG	GAG	ACA	GCC	CAG	GGC	CTT	GAT	GGG	CAC	AGC	CAT	CTT	1327
V	M	Y	L	G	T	T	T	G	S	L	H	K	A	V	V	S	G	D	S	452
GTC	ATG	TAC	CTG	GGA	ACC	ACC	ACA	GGG	TCG	CTC	CAC	AAG	GCT	GTG	GTA	AGT	GGG	GAC	AGC	1387
S	A	H	L	V	E	E	I	Q	L	F	P	D	P	E	P	V	R	N	L	472
AGT	GCT	CAT	CTG	GTG	GAA	GAG	ATT	CAG	CTG	TTC	CCT	GAC	CCT	GAA	CCT	GTT	CGC	AAC	CTG	1447
Q	L	A	P	T	Q	G	A	V	F	V	G	F	S	G	G	V	W	R	V	492
CAG	CTG	GCC	CCC	ACC	CAG	GGT	GCA	GTG	TTT	GTA	GGC	TTC	TCA	GGA	GGT	GTC	TGG	AGG	GTG	1507
P	R	A	N	C	S	V	Y	E	S	C	V	D	C	V	L	A	R	D	P	512
CCC	CGA	GCC	AAC	TGT	AGT	GTC	TAT	GAG	AGC	TGT	GTG	GAC	TGT	GTC	CTT	GCC	CGG	GAC	CCC	1567
H	C	A	W	D	P	E	S	R	T	C	C	L	L	S	A	P	N	L	N	532
CAC	TGT	GCC	TGG	GAC	CCT	GAG	TCC	CGA	ACC	TGT	TGC	CTC	CTG	TCT	GCC	CCC	AAC	CTG	AAC	1627

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Fig. 3C

S	W	K	Q	D	M	E	R	G	N	P	E	W	A	C	A	S	G	P	M	552
TCC	TGG	AAG	CAG	GAC	ATG	GAG	CGG	GGG	AAC	CCA	GAG	TGG	GCA	TGT	GCC	AGT	GGC	CCC	ATG	1687
S	R	S	L	R	P	Q	S	R	P	Q	I	I	K	E	V	L	A	V	P	572
AGC	AGG	AGC	CTT	CGG	CCT	CAG	AGC	CGC	CCG	CAA	ATC	ATT	AAA	GAA	GTC	CTG	GCT	GTC	CCC	1747
N	S	I	L	E	L	P	C	P	H	L	S	A	L	A	S	Y	Y	W	S	592
AAC	TCC	ATC	CTG	GAG	CTC	CCC	TGC	CCC	CAC	CTG	TCA	GCC	TTG	GCC	TCT	TAT	TAT	TGG	AGT	1807
H	G	P	A	A	V	P	E	A	S	S	T	V	Y	N	G	S	L	L	L	612
CAT	GGC	CCA	GCA	GCA	GTC	CCA	GAA	GCC	TCT	TCC	ACT	GTC	TAC	AAT	GGC	TCC	CTC	TTG	CTG	1867
I	V	Q	D	G	V	G	G	L	Y	Q	C	W	A	T	E	N	G	F	S	48 / 96
ATA	GTG	CAG	GAT	GGA	GTT	GGG	GGT	CTC	TAC	CAG	TGC	TGG	GCA	ACT	GAG	AAT	GGC	TTT	TCA	632
Y	P	V	I	S	Y	W	V	D	S	Q	D	Q	T	L	A	L	D	P	E	1927
TAC	CCT	GTG	ATC	TCC	TAC	TGG	GTG	GAC	AGC	CAG	GAC	CAG	ACC	CTG	GCC	CTG	GAT	CCT	GAA	652
L	A	G	I	P	R	E	H	V	K	V	P	L	T	R	V	S	G	G	A	1987
CTG	GCA	GGC	ATC	CCC	CGG	GAG	CAT	GTG	AAG	GTC	CCG	TTG	ACC	AGG	GTC	AGT	GGT	GGG	GCC	672
A	L	A	A	Q	Q	S	Y	W	P	H	F	V	T	V	T	V	L	F	A	2047
GCC	CTG	GCT	GCC	CAG	CAG	TCC	TAC	TGG	CCC	CAC	TTT	GTC	ACT	GTC	ACT	GTC	CTC	TTT	GCC	692
L	V	L	S	G	A	L	I	I	L	V	A	S	P	L	R	A	L	R	A	2107
TTA	GTG	CTT	TCA	GGA	GCC	CTC	ATC	ATC	CTC	GTG	GCC	TCC	CCA	TTG	AGA	GCA	CTC	CGG	GCT	712
																				2167

Fig. 3D



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R   G   K   V   Q   G   G   C   E   T   L   R   P   G   E   K   A   P   L   S   R   732
CGG GGC AAG GTT CAG GGC TGT GAG ACC CTG CGC CCT GGG GAG AAG GCC CCG TTA AGC AGA 2227

E   Q   H   L   Q   S   P   K   E   C   R   T   S   A   S   D   V   D   A   D   752
GAG CAA CAC CTC CAG TCT CCC AAG GAA TGC AGG ACC TCT GCC AGT GAT GTG GAC GCT GAC 2287

N   N   C   L   G   T   E   V   A   *
AAC AAC TGC CTA GGC ACT GAG GTA GCT TAA
                                     762
                                     2317

ACTCTAGGCACAGGCCGGGCTGCCGTGCAGGCACCTGGCCCATGCTGGCTGGCGGGCCCAAGCACAGCCCTGACTAGGA 2396
TGACAGCAGCACAAAAGACCACTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCTACTCATCTGATGACACTCAGCAGGG 2475
TGATGCACAGCAGTCTGCCCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGCTACCC 2554
CCAGACCTGCTCCTACACTGATATTGAAGAAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCTCCAGAAA 2633
CACAGTGTTCAGAGATCCTAAAAAACCTGCCCTGTCCCAGGACCCCTATGGTAATGAACACCCAAACATCTAAACAATC 2712
ATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCA 2791
TGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCCGCTGACTCCCAGGAAGTCTTCTCTGAAGTCTGACC 2870
ACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTTGGCAGAAATGGCAGGGGTAATCTGAGCCTTCT 2949
TCACTCCTTTACCCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCCTTTTGGGATTTCAGAAAACTGCTTGTG 3028
AGAGACTGTTTATTTTATTAAAAATATAAGGCTTAAAAAAAATAAAAAAAAAGGGGCGCGC 3104

```

Fig. 3E

Hum.	10	20	30	40	50	60	70
	MALPALGDPWSLLGLFLFQLLQLLPTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLS						
	.....	.....	.....	.....	.....	.....	.....
Mur.	10	20	30	40	50	60	70
	MALPSLGQDSWSLLRVFFQLFLPSLPASGTGGQGPMPRVKYHAGDGHRALESFFQKGLRDFDTLLS						
	.....	.....	.....	.....	.....	.....	.....
Hum.	80	90	100	110	120	130	140
	GDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLY						
	.....	.....	.....	.....	.....	.....	.....
Mur.	80	90	100	110	120	130	140
	DDGNTLYVGARETVLALNIQNPPIPRLKNMIPWPASERKKTECAFKKKSNETQCFNFIRVLVSYNATHLY						
	.....	.....	.....	.....	.....	.....	.....
Hum.	150	160	170	180	190	200	210
	TCGTFAFSPACTFIELQDSYLLPISEDKVMEKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMR						
	.....	.....	.....	.....	.....	.....	.....
Mur.	150	160	170	180	190	200	210
	ACGTFAFSPACTFIELQDSLLPILIDKVMGKGQSPLTFTSTQAVLVDGMLYSGTMNFLGSEPILMR						
	.....	.....	.....	.....	.....	.....	.....
Hum.	220	230	240	250	260	270	280
	TLGSQPVLKTDFLRWLHHDASFVAaipSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQ						
	.....	.....	.....	.....	.....	.....	.....
Mur.	220	230	240	250	260	270	280
	TLGSHPVLKTDFLRWLHADASFVAaipSTQVVYFFFEETASEFDFFEEELYISRVAQVCKNDVGGEKLLQ						
	.....	.....	.....	.....	.....	.....	.....

Fig. 3F

Hum.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCTQPGQLPENVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
Mur.	290	300	310	320	330	340	350
	KKWTTFLKAQLLCAQPGQLPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLTDIERVF						
Hum.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV						
Mur.	360	370	380	390	400	410	420
	KGKYKELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFMDHVVVGTPLLVKSGVEYTRLAV						
Hum.	430	440	450	460	470	480	490
	ETAQGLDGHSHLVMYLGTGTTGSLHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGA VFGFSGGVW						
Mur.	430	440	450	460	470	480	490
	ESARGLDGSSHVVMYLGTSTGPLHKAVVPQDSSAYLVEEIQLSPDSEPVRLQLAPAQGA VFAFGSGGIW						
Hum.	500	510	520	530	540	550	560
	RVPRANC SVYESCVDCVLARDPHCAWDPESTRCTCLLSAPNLSWKQDMERGNPEWACASGPMRSRLRPQS						
Mur.	500	510	520	530	540	550	560
	RVPRANC SVYESCVDCVLARDPHCAWDPESTRCLLSGST-KPWKQDMERGNPEWVCTRGPMA RSPRRQS						

Fig. 3G

Hum.	570	580	590	600	610	620	630
	RPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLI	VQDGVGGLYQCWATENG					
	.....	.....	.....	.....	.....	.....	.....
Mur.	560	570	580	590	600	610	620
	PPOLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKISEASATVYNGSLLLPQDGVGGLYQCVATENG						
	.....	.....	.....	.....	.....	.....	.....
Hum.	640	650	660	670	680	690	700
	FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVT	VLFAVLGALI					
	.....	.....	.....	.....	.....	.....	.....
Mur.	630	640	650	660	670	680	690
	YSYPVVSYWVDSQDQPLALDPELAGVPRERVQVPLTRVGGASMAAQRSYWPHFLI	VTVLLAIVLLGVLT					
	.....	.....	.....	.....	.....	.....	.....
Hum.	710	720	730	740	750	760	
	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASD	VDADNNCLGTEVA					
	.....	.....	.....	.....	.....	.....	.....
Mur.	700	710	720	730	740	750	760
	LLASPLGALRARGKVQCGMLPPREKAPLSRDQHLQPSKDHRTSASD	VDADNNHLGAEVA					
	.....	.....	.....	.....	.....	.....	.....

Fig. 3H

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Hum.  GTCG-AC-CC-----ACG-----CGTCCGGT-----CTGTGGCTGAGCATGGC
      :: :: ::
Mur.  CTCGACGCCCTGGGTTAGGGTCTGTACTGTCTGGGGAACCATCTGGTGACCATCTCAGGCTGACCATGGC
      10  20  30  40  50  60  70
      :: :: ::
      40  50  60  70  80  90  100
Hum.  CCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCCCTTTCTCTCTTCCAACTGCTTC-AGCTGCT
      :: :: ::
Mur.  CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTCTTCCAACT-CTTCCTGCTGCC
      80  90  100  110  120  130
      110  120  130  140  150  160  170
Hum.  GCTGCCGACGACACCGCGGGGGAGCGGGCAGGGGCCCATGCCCCAGGGTCAGATATACTATGCAGGGGAT
      . . . . .
Mur.  ATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCCCAGAGTCAAATACCATGCTGGAGAC
      140  150  160  170  180  190  200
      180  190  200  210  220  230  240
Hum.  GAACGTAGGGCACTTAGCTTCTTCCACCAGAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTG
      :...:
Mur.  GGGCACAGGGCCCTCAGCTTCTTCCAAACAAAGGCCCTCCGAGACTTTGACACGCTGCTCCTGAGTGACG
      210  220  230  240  250  260  270

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Fig. 3II

File 31

	530	540	550	560	570	580	590
Hum.	GGAGGACAAGGTCATGGAGGGA	AAAGGCCAAGCCCTTTGACCCCGCTCACAAGCATACG-GCTGTCTT					
	.....	.....	.....	.....	.....	.....	.....
Mur.	GATAGACAAGGTCATGGACGGGAAGGCCAAAGCCC-TTTGACCCCTGTTCAACAAGCACACAAGCTGTCTT						
	560	570	580	590	600	610	620

	600	610	620	630	640	650	660
Hum.	GGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC	TTCCTGGCAGTGAGCCCATCCTGATGCGCAC					
	:::	:::	:::	:::	:::	:::	:::
Mur.	GGTCGATGGGATGCTTTATTCCGGCACCATGAACAAC	TTCCTGGCAGCGAGCCCATCCTGATGCGGACA					
	630	640	650	660	670	680	690

	670	680	690	700	710	720	730
Hum.	CTGGGATCCCAGCCTGTCTCAAGACCGACAAC	TCTCCGCTGGCTGCATCATGACGCC	TCTTGTGG				
	::::::::::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::
Mur.	CTGGGATCCCATCCTGTTCTCAAGACTGACATCT	TCTTACGCTGGCTGCACGGGATGCC	TCTTCGTGG				

	740	750	760	770	780	790	800
Hum.	CAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCGAGGAGACAGCCAGCGAGTTGACTTCTTTGA						
	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
Mur.	CAGCCATTCCATCCACCAGGTCGTCTATTCTTCTTTGAGGAGACAGCCAGCGAGTTGACTTCTTTGA						
	770	780	790	800	810	820	830

Fig. 3K

	810	820	830	840	850	860	870
Hum.	GAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGCGGCGGAAAAGCTGCTGCAGAAG						
	..... : : :: : .....						
Mur.	AGAGCTGTATATATCCAGGTGGCTCAAGTCTGCAAGAACGACGTGGCGGTGAAAAAGCTGCTGCAGAAG						
	840	850	860	870	880	890	900
Hum.	AAGTGGACCACCTTCCTGAAGGCCAGCTGCTCTGCACCCAGCCGGGCGAGCTGCCCTTCAACGTCATCC	880	890	900	910	920	930
	..... : .....						
Mur.	AAGTGGACCACCTTCCTCAAAGCCCAGTTGCTCTGCGCTCAGCCAGGCGAGTGCCATTCAACATCATCC						
	910	920	930	940	950	960	970
Hum.	GCCACGCGGTCTGCTCCCCGCCGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTG	950	960	970	980	990	1000
	..... : .....						
Mur.	GCCACGCGGTCTGCTGCCCGCCGATTCTCCCTCTGTTTCCCGCATCTACGCAGTCTTTACCTCCCAGTG						
	980	990	1000	1010	1020	1030	1040
Hum.	GCAGGTTGGCGGGACCAAGGAGCTCTGCGGTTTGTCCTTCTCTCTTGACATTTGAACGTGCTTTAAG	1020	1030	1040	1050	1060	1070
	..... : .....						
Mur.	GCAGGTTGGCGGGACCAAGGAGCTCAGCAGTCTGTGCTTCTCTCTCACGGACATTGACCGAGTCTTTAA						
	1050	1060	1070	1080	1090	1100	1110

Fig. 3L



**Fig. 3M**



30  
File

	1930	1940	1950	1960	1970	1980	1990
Hum.	TCATACCCCTGTGATCTCCTACTGGGTGACAGCAGGACACCCCTGGCCCTGGATCCTGAACCTGGCAG						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	TCATACCCCTGTGGTCTCCTATTGGGTAGACAGCAGGACACCCCTGGCGCTGGACCCCTGAGCTGGCGG						
	1960	1970	1980	1990	2000	2010	2020
	2000	2010	2020	2030	2040	2050	2060
Hum.	GCATCCCCCGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCA						
	::::	::::	::::	::::	::::	::::	::::
Mur.	GCGTTCCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGGGAGCTTCCATGGCTGCCAGCG						
	2030	2040	2050	2060	2070	2080	2090
	2070	2080	2090	2100	2110	2120	2130
Hum.	GTCCCTACTGGCCCCACCTTTGTCACTGTCACTGTCTCTTTGCCCTTAGTGCTTTCAGGAGCCCTCATCATC						
	::::::::::	::::	::::	::::	::::	::::	::::
Mur.	GTCCCTACTGGCCCCCATTTTCTCATCGTTACCGTCCCTCCTGGCCATCGTGCTCCTGGAGTGCTCACTCTC						
	2100	2110	2120	2130	2140	2150	2160
	2140	2150	2160	2170	2180	2190	2200
Hum.	CTCGTGGCCTCCCCCATTTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAAGGCTGTGAGACCCCTGCGCCCTG						
	::::	::::	::::	::::	::::	::::	::::
Mur.	CTCCTCGCTTCCCCACTGGGGCGCTGCGGGCTCGGGGTAAGTTCAAGGCTGTGGGATGCTGCCCCCA						
	2170	2180	2190	2200	2210	2220	2230

Fig. 3P

	2210	2220	2230	2240	2250	2260	2270
Hum.	GGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA						
	2240	2250	2260	2270	2280	2290	2300
Mur.	GGGAAAAGGCTCCACTGAGCAGGACCAGCACCTCCAGCCCCTCCAAGGACCACAGGACCTCTGCCAGTGA						
	2280	2290	2300	2310	2320	2330	2340
Hum.	TGTGACGCTGACAACAACACTGCCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGG-CCGGGGCTG--C						
	2310	2320	2330	2340	2350	2360	2370
Mur.	CGTAGATGCCGACACAACCACTCTGGCGCCGAAAGTGGCTTAAACA-GGGACACAGATCCGCAGCTGAGC						
	2350	2360	2370	2380	2390	2400	2410
Hum.	GGTGCAGGCACCTGGCCATGCTGGCTGGCGGCCCAAGCACAGCCCTGACTAGATGACAGCAGCAAAA						
	2380	2390	2400	2410			
Mur.	AGAGCAAGCCACTGGCCTTGTGGCTATGC---CAGGCACAG-----TGCCACTCT--						
	2420	2430	2440	2450	2460	2470	2480
Hum.	AGACCACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGC						
	2430	2440	2450	2460	2470	2480	
Mur.	-GACCA-----GGGTAGGAG--GCT-CT-C-CTGCTA-ACGTGTGTCAC-CTACAG-----C						

Fig. 3Q



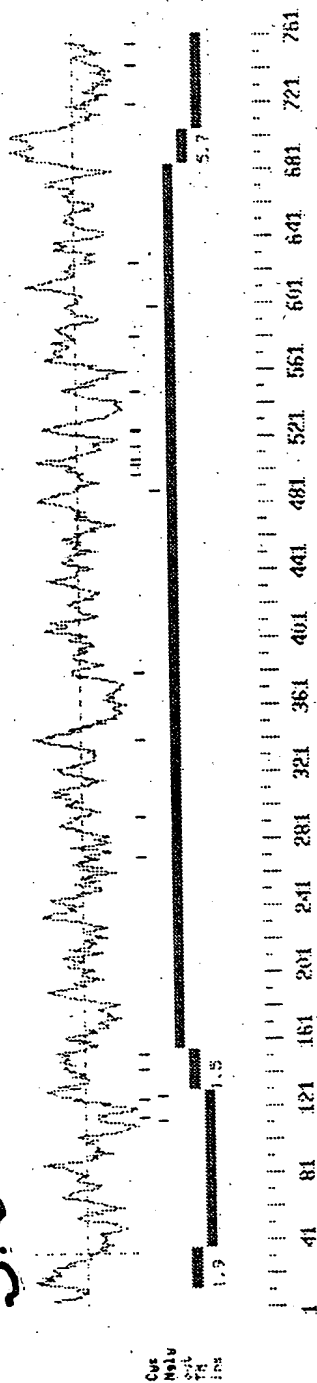
	2760	2770	2780	2790	2800	2810
Hum.	----GCTGCCGCTTTGGACACCAACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC					
	2730	2740	2750	2760	2770	2780
Mur.	AGCAGCTGCTGCTTTGAACACACAGCCCCCTCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT					
	2820	2830	2840	2850	2860	2870
Hum.	TTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACTTTCTTCTTGC					
	2800	2810	2820	2830	2840	2850
Mur.	TTCCCTTACCAGTCGGGCCATACTGTTT---GGGAAGTCACTCTGAAGTCTAACCACTTCTCTCTTG					
	2890	2900	2910	2920	2930	2940
Hum.	TTCAGTTGGGCAGACTCTGATCCCT---TCTGCCCTGGCAGAAATGCAGGGTAATCTGAGCCTTCTTC					
	2860	2870	2880	2890	2900	2910
Mur.	TTCAGTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAGAAATGGGGGCATAATCTGAGCCTTGTTTC					
	2960	2970	2980	2990	3000	3010
Hum.	ACTCCCTTACCC---TAGCTGACCCCTTCACCTCTCCC--CCTCCCTTTTCCCTTGTTTGGGATTCAGA					
	2930	2940	2950	2960	2970	2980
Mur.	---CCTTGTCAGTGTGGCTGACCC-TTGACCTCTTTCCTTCCTCC---TCCCTTGTTTTGGGATTCAGA					

Fig. 3S

**Fig. 3T**



Fig. 3U



GTCGACCCACGCGTCCGCGGACGCGTGGGACGGCTCCCGGCTGCAGTCTGCCCGCCCCCGCGGGGCCGAGTC	79
CGGAAGCGCGCTGCGACCCGCGTCCGGCGCTGGAGAGGACGCGAGAGCC	152
K V A A L L L G L L L E C T E A K K H C	6
AAG GTG GCG GCG CTG CTC GGG CTG CTC TTG GAG TGC ACA GAA GCC AAA AAG CAT TGC	212
W Y F E G L Y P T Y Y I C R S Y E D C C	46
TGG TAT TTC GAA GGA CTC TAT CCA ACC TAT TAT ATA TGC CGC TCC TAC GAG GAC TGC TGT	272
G S R C C V R A L S I Q R L W Y F W F L	66
GGC TCC AGG TGC TGT GTG CGG GCC CTC TCC ATA CAG AGG CTG TGG TAC TTC TGC TTT CTT	332
L M M G V L F C C G A G F I R R R M Y	86
CTG ATG ATG GGC GTG CTT TTC TGC TGC GGA GCC GGC TTC TTC ATC CGG AGG CGC ATG TAC	392
P P P L I E E P A F N V S Y T R Q P P N	106
CCC CCG CCG CTG ATC GAG GAG CCA GCC TTC AAT GTG TCC TAC ACC AGG CAG CCC CCA AAT	452
P G P G A Q Q CAG CAG CCG GGG CCG CCC TAT TAC ACT GAC CCA GGA GGA CCG GGG	126
CCC GGC CCA GGA GCC CAG CAG CCG GGG CCG CCC TAT TAC ACT GAC CCA GGA GGA CCG GGG	512
M N P V G N S M A M A F Q V P P N S P Q	146
ATG AAC CCT GTC GGC AAT TCC ATG GCA ATG GCT TTC CAG GTC CCA CCC AAC TCA CCC CAG	572

Fig. 4A

G S V A C P P P P A Y C N T P P P P Y E 166  
 GGG AGT GTG GCC TGC CCG CCT CCA GCC TAC TGC AAC ACG CCT CCG CCC CCG TAC GAA 632

Q V V K A K \* 173  
 CAG GTA GTG AAG GCC AAG TAG 653

TGGGGTGCCACGTGCAAGAGGAGACAGGAGGGCCCTTCCCTGGCCCTTCTGTCTTCGTTGATGTTCACTTCCAG 732  
 GAACGGTCTCGTGGGCTGCTAAGGCAGTTCCCTCTGATATCCTCACAGCAAGCACAGCTCTCTTTCAGGCTTCCATGG 811  
 AGTACAATATATGAACCTCACACTTTGTCTCCCTCTGTCTTCTGTCTTCTGACGCAGTCTGTGCTCTCACATGGTAGTGT 890  
 GGTGACAGTCCCCGAGGGCTGACGTCCTTACGGTGGCGTGACCAAGATCTACAGGAGAGAGACTGAGAGGAAGAGGCAG 969  
 TGCTGGAGGTGCAGGTGGCATGTAGAGGGCCAGGCCGAGCATCCAGGCAAGCATCCTTCTGCCCCGGTATTAATAGG 1048  
 AAGCCCCATGCCCCGGGCTCAGCCGATGAAGCAGCAGCCGACTGAGCTGAGCCCCAGCAGTCACTGCTCCAGCCCTGT 1127  
 CCTCTCGTCAGCCTTCCCTTCCAGAAGCTGTTGGAGAGACATTCAGGAGAGAGCAAGCCCTTGTCTGTCTGTCT 1206  
 CTGTTCATATCCTAAAGATAGACTTCTCTGCACCCGAGGAAAGGTAGCACGTGCAGCTCTCACCGCAGGATGGGGC 1285  
 CTAGAAATCAGGCTTGCCCTTGGAGGCCCTGACAGTGATCTGACATCCACTAAGCAAAATTTATTTAAATTCATGGGAAATCA 1364  
 CTTCCCTGCCCCAAACTGAGACATTGCATTTTGTGAGCTCTTGGTCTGATTTGGAGAAAGGACTGTTACCCATTTTTTTG 1443  
 GTGTGTTTATGGAAGTGCAATGAGCGTCCCTGCCCTTTGAAATCAGACTGGGTGTGTCTTCCCTGGACATCACTGC 1522  
 CTCCTCAGGGCATTCACGGCCCCGGGGTCTCCTTCCCTCAGGCAGCTCCAGTGGTGGTCTCTGAAGGGTGCTTTTCAAA 1601  
 ACGGGGCACATCTGGCTGGGAAGTCACATGGAATCTTCCAGGGAGAGAGACCAGCTGAGGCGTCTCTCTCTGAGGTTGT 1680  
 GTTGGGCTAAAGCGGGTGTGTGCTGGGCTCCAAGGAGGAGAGCTTGTCTGGGAAAGACAGGAGAACTGACTCAAC 1759  
 TGCACTGACCATGTTGTCAATAATTAGAAATAAAGAAAGAGTGTCGGAAATGCACATTCCTGGATAGGAATCACAGCTCA 1838  
 CCCCAGGATCTCACAGGTAGTCTCCTGAGTAGTTGACGGCTAGCGGGGAGCTAGTTCCGCCGCATAGTTATAGTGTGA 1917  
 TGTGTGAACGCTGACCTGTCCCTGTGTGCTAAGAGCTATGCAGCTTAGCTGAGGCGCCTAGATTACTAGATGTCTGTAT 1996  
 CACGGGAATGAGGTGGGGTGTCTTATTTTAAATGAACATAATCAGAGCCCTCTTGAGAAAATTGTTACTCATTTGAACCTGG 2075  
 AGCATCAAGACATCTCATGGGAAGTGGATACGGAGTGATTTTGGTGTCCATGTCTTTTCACTCTGTAGGACATTTAATCGGAG 2154

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Fig. 4B

AACCTCCTGGGGAATTTGTGGGAGACACTTGGGAACAAAAACAGACACCCCTGGGAATGCAGTTGCAAGCACAGATGCTG 2233  
 CCACCAAGTGCTCTGACCAACCCCTGGTGACTGCTGACTGCCAGCGTGGTACCTCCCATGTCTGCAGGCCCTCCATCTAAA 2312  
 TGAGACAACAAAGCACAAATGTTCACTGTTTACAACCAAGACAACCTGCGTGGTCCAAACACTCCTCTTCCTCCAGGTCA 2391  
 TTTGTTTGGCAATTTTAAATGCTCTTTAATTTTTGTAAATGAAAAAGCACACTAAGCTGCCCTGGAAATCGGGTGCAGCTGA 2470  
 ATAGGCACCCAAAAGTCCGTGACTAAATTTTCGTTTGTCTTTTGTATAGCAAAATTATGTTAAGAGACAGTATGGCTAGG 2549  
 GCTCAACAATTTGTATTTCCCATGTTTGTGTGAGACAGAGTTTGTTTTCCCTTGAACCTTGGTTAGAATTGTGCTACTGT 2628  
 GAACGCTGATCCTGCATATGGAAGTCCCACTTTGGTGACATTTTCTGGCCATTCTTGTTCATTGTGTGATGGTGGG 2707  
 TTGTGCCCCACTTCCTGGAGTGAGACAGCTCCTGGTGTAGAAATTTCCCGGAGCGTCCGTGTTTCAGAGTAAACTTGAAG 2786  
 CAGATCTGTGCATGCTTTTCCCTCTGCAACAATTGGCTCGTTTCTCTTTTGTCTCTTTTGTATAGGATCCTGTTTCCT 2865  
 ATGTGTGCAAAATAAAAAATAAATTGGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2944  
 AAAAAAAGGGCGGCGCGC 2964

Fig. 4C

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GTCGACCCACGCGTCCGGCGCGCGTCTTCTGCGGGCTTCAGCTCGTATCCCCGGAGTCCACCCGCCCGTCCCGGGGT 79  
 GCGGACTGGCCCTGAGCTGGCCGTACAGCCCCGGCTTCGGACGGTCTCGCTGGAGCC ATG GGC CGC CGG CTC 151  
 M G R R L 5  
 G R V A A L L L L G L L V E C T E A K K H 25  
 GGC AGG GTG GCG CTG CTG CTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT 211

Fig. 4D

C	W	Y	F	E	G	L	Y	P	T	Y	Y	I	C	R	S	Y	E	D	C	45
TGC	TGG	TAT	TTT	GAA	GGA	CTC	TAT	CCC	ACA	TAC	TAT	ATA	TGC	CGT	TCC	TAT	GAA	GAC	TGC	271
C	G	S	R	C	C	V	R	A	L	S	I	Q	R	L	W	Y	F	W	F	65
TGT	GGC	TCC	AGG	TGC	TGT	GTG	AGG	GCC	CTT	TCC	ATA	CAG	AGG	CTG	TGG	TAT	TTT	TGG	TTC	331
L	L	M	M	G	V	L	F	C	C	G	A	G	F	F	I	R	R	R	M	85
CTG	CTG	ATG	ATG	GGT	GTG	CTG	TTC	TGC	TGT	GGT	GCC	GGT	TTC	TTC	ATT	CGC	CGG	CGC	ATG	391
Y	P	P	P	L	I	E	E	P	T	F	N	V	S	Y	T	R	Q	P	P	105
TAT	CCG	CCA	CCA	CTC	ATT	GAG	GAG	CCC	ACA	TTC	AAT	GTG	TCC	TAT	ACC	AGG	CAG	CCA	CCA	451
N	P	A	P	G	A	Q	Q	M	G	P	P	Y	Y	T	D	P	G	G	P	125
AAT	CCT	GCT	CCA	GGA	GCA	CAG	CAA	ATG	GGA	CCG	CCA	TAT	TAC	ACC	GAC	CCT	GGA	GGA	CCC	511
G	M	N	P	V	G	N	T	M	A	M	A	F	Q	V	Q	P	N	S	P	145
GGG	ATG	AAT	CCT	GTT	GGC	AAT	ACC	ATG	GCT	ATG	GCT	TTC	CAG	GTC	CAG	CCC	AAT	TCA	CCT	571
H	G	G	T	T	Y	P	P	P	P	S	Y	C	N	T	P	P	P	P	Y	165
CAC	GGA	GGC	ACA	ACT	TAC	CCA	CCC	CCT	CCT	TCC	TAC	TGC	AAC	ACG	CCT	CCA	CCC	CCC	TAT	631
E	Q	V	V	K	D	K	*													173
GAA	CAG	GTG	GTG	AAG	GAC	AAG	TAG													655
CAAGATGCTACATCAAAGGCAAGAGGATGGACAGGCCCTTTTGTGTTACCTTCCCATCCTCACCAGATACTTGCTGATAG																				734

Fig. 4E

GGTGGTCC AAGGAA AACTTGGATA TTTCTCAA AGCAAGCC CAGCTCTCTTTCAA GTCCTTTTGTGG AGGACATTTGAATC 813  
CACACTGTCT CCTCTGTTGCTTCTGTATGTAGTCTCTGTGCTCTCTGAGAGAGTGTGGCAACAGTCCCCTGAGGGTT 892  
GATATTCCTAGGGTGTCCAGGTAGATCCTCGGAGAGAGGCTAAGGGAAAGGAAGCATAGCCTGTGTGTAGGGGG 971  
CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACCTTCGAAGAGACACTATCCACCA 1050  
TCCCAGCCCATTTCTCCTAATAGAAGCTGTGGGGCTGTGTTGTTGATGCTCTTTTGGTCTCCACTCACATTTTGAAAAATAG 1129  
GCTTTCCCTCTGCAGGAATAGGAAAGACCCAAAGTACATAATTTGCTTCCACTTAAAAATGAGGGTCAGAACCAGGCCCTCAG 1208  
TTGGACATCTATAGTTAAATAAAGGCCATTAGAGAGGGGAAATCTTTAAGTTAGGGGAAATTTCTAAATGGAGACATT 1287  
GCGTTTATGAATCATCGTCTGGCTTTTCTTTTAGTGCAATGTAATTGAAGTGAGGGTGTCCCTTTTGAGATCAGATGGGGAG 1366  
AGTGAAC TCTCGGGGGGTGGGTGTCTCTACTCAGAGGGCTCCAAACACCCCTTTTCTTAGGTAGTTCTGGTGATGGGTT 1445  
TTATGGC ACTATAGAGCTGAGGGGCACATTAGGCCGGGTAGTTACATTTGACCCCTTGAGAGGAAGAGGACAGCCAAAG 1524  
AAACTCAGCAAAGCAAGACCAAGCATTTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCAACAGAGATGTGCTGCCCTCA 1603  
GAAGAGGGGACGTTTGTGGATAGAGCCGTGAAAAACCTACTTAGTTGCACAGATGACATAATCAAAAAGTAGAGAAAGAAG 1682  
TGTAGTTAGAGATGCCATTTCCAGGTGAGAAATCAGAGCTCATCCATAGATTTACAAGTAGTGGCTGGAGTTAACAGTA 1761  
TGGAGTTCTTTCCCTTGGCTAGTTAGTCACGTTGATGTGTATTTAAACCCAGGTTGAGACCTTGTGTACTAAGAGCAA 1840  
GGAAGTATAGCTAAGATGTCTAGATTATTTATATGTAGTATGGTGGGGAGTGGGGCTGCAAGGAAGGGGCTGACATTG 1919  
TAAATGAGAAAATCAGAGCCATTTGATAAACTGTTACTTGTGGATCAGGCATCCAAAAGTGTCTCTTGAGTGGACATT 1998  
GAGTATTCCTTACCACCTACAAGACCAGGAGGCATGGTGTCTCTCCATTGGGGTATTTATATGAGGTAGAGGTTTCAAG 2077  
GAATCGACAGTAGCTGTGGCTTAGTTTAAGGACTGAAAGCATAGGGACTGGTAGACAGTTTCATAGGAAACTGCGG 2156  
GGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCATCATTTGAGCACCCCTTGTGTCTCTGGC 2235  
TTCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGTCCCTTGTGTTTACATAAGACACAAGCACAAATGTCTGCTGTT 2314  
TACAAATCAAGACGACTACATGGTCCAAACATTTCTCTCTCTATCACTTGTGGCTTTAACTTCCATTTCCCTCCGTT 2393  
CCTTTTAAAAATCAAGAAGCACAGTCAGAGCTGCCCTGGGATTTGCATCAGGGAACGGCTGATCAAGGCATTCAGTGTC 2472  
CATGACTAAATCTTATCTTTTGTATAGCAAAATCCTTTTAAGAAAATGAACAATTTGCTAAGGCTCAGCAATTTTATACTC 2551  
CAATGCTGTGAAGGTAAATTTGTTTGGCCATTGAGCCACATTTGGAATTCCTTCTGACGTCAACACTGACAATGCSCT 2630  
ATGGAAATTGCACTTCTGGGTATATGTCCAGCATCCTTGTGTTTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC 2709

Fig. 4F

AGCTCTACTTCTGTGCTGAGGTCCTGTAGAGCCGGGGCTTGGGCACAGACATGAGGCAGACTTGTGCATGCTCTTTC 2788  
 TTGGCAACACTTGGCTCATATTCTTGTCTCTTTTGATAGAGTCCTGTTTCCATGTATTTAAAAAATAATAAAGTG 2867  
 AATTAGTCAAAAAAATAAAAAAATAAAAAAAGGCGGCCGC 2915

Fig. 4G

	10	20	30	40	50	60	70
Hum.	MRRQPAKVAALLGLLLECTEAKKHCWFEGLYPTYICRSYEDCCGSRCCVRALS	QRLWYFWFLMMG					
	:	:	:	:	:	:	:
Mur.	MGRRLGRVAALLGLLVECTEAKKHCWFEGLYPTYICRSYEDCCGSRCCVRALS	QRLWYFWFLMMG					
	10	20	30	40	50	60	70

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	80	90	100	110	120	130	140
Hum.	VLFCGAGFFIRRRMYPPPLIEEPAFNVS	YTRQPNPGPQAQQPGPPYYTD	PGGPMN	PVGN	SMA	MAFQV	
	:	:	:	:	:	:	:
Mur.	VLFCGAGFFIRRRMYPPPLIEEPTFNVS	YTRQPNPAPQAQQMGPPYYTD	PGGPMN	PVGN	TM	MAFQV	
	80	90	100	110	120	130	140

	150	160	170
Hum.	PPNSPQGSVACPPPPAYCNT	PPPPYEQVVKAK	
	:	:	:
Mur.	QPNSPHGGTTYPPPPSYCNT	PPPPYEQVVKDK	
	150	160	170

Fig. 4H

004250"E9082560

Fig. 4I

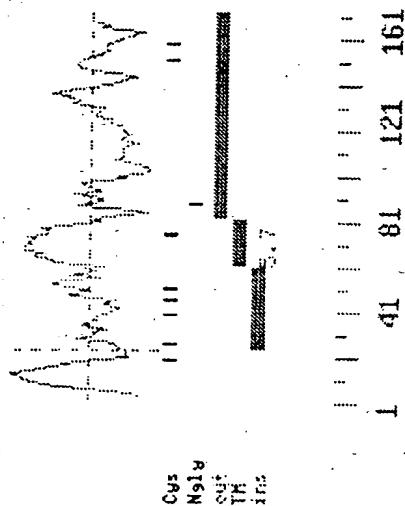
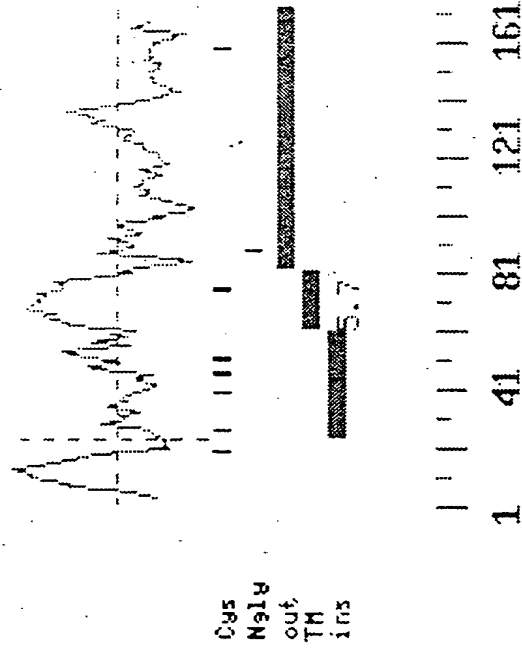




Fig. 4J



GTCGACCCACGGTCCGACGCTTTGGACACTTCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCAACTAAAGGA	79
M C T K T I	
TCAAGAAAGGCCAGCACAGCAGAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC	150
P V L W G C F L L W N L Y V S S S Q T I	26
CCA GTC CTC TGG GGA TGT TTC CTC CTG TGG AAT CTC TAT GTC TCA TCC TCT CAG ACC ATT	210
Y P G I K A R I T Q R A L D Y G V Q A G	46
TAC CCT GGA ATC AAG GCA AGG ATT ACT CAG AGG GCA CTT GAC TAT GGT GGT CAA GCT GGA	270
M K M I E Q M L K E K K L P D L S G S E	66
ATG AAG ATG ATT GAG CAA ATG ATG CTA AAA GAA AAG AAA CTC CCA GAT TTA AGC GGT TCT GAG	330
S L E F L K V D Y V N Y N F S N I K I S	86
TCT CTT GAA TTT CTA AAA GTT GAT TAT GTA AAC TAC AAT TTT TCA AAT ATA AAA ATC AGT	390
A F S F P N T S L A F V P G V G I K A L	106
GCC TTT TCA TTT CCA AAT ACC TCA TTG GCT TTT GTG CCT GGA GTG GGA ATC AAA GCG CTA	450
T N H G T A N I S T D W G F E S P L F V	126
ACC AAC CAT GGC ACT GCC AAC ATC AGC ACA GAC TGG GGG TTC GAG TCT CCA CTT TTT GTT	510
L Y N S F A E P M E K P I L K N L N E M	146
CTG TAT AAC TCC TTT GCT GAG CCC ATG GAG AAA CCC ATT TTA AAG AAC TTA AAT GAA ATG	570

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Fig. 5A

L C P I I A S E V K A L N A N L S T L E	166
CTC TGT CCC ATT ATT GCA AGT GAA GTC AAA GCG CTA AAT GCC AAC CTC AGC ACA CTG GAG	630
V L T K I D N Y T L L D Y S L I S S P E	186
GTT TTA ACC AAG ATT GAC AAC TAC ACT CTG CTG GAT TAC TCC CTA ATC AGT TCT CCA GAA	690
I T E N Y L D L N L K G V F Y P L E N L	206
ATT ACT GAG AAC TAC CTT GAC CTG AAC TTG AAG GGT GTA TTC TAC CCA CTG GAA AAC CTC	750
T D P P F S P V P F V L P E R S N S M L	226
ACC GAC CCC CCC TTC TCA CCA GTT CCT TTT GTG CTC CCA GAA CGC AGC AAC TCC ATG CTC	810
Y I G I A E Y F F K S A S F A H F T A G	246
TAC ATT GGA ATC GCC GAG TAT TTC TTT AAA TCT GCG TCC TTT GCT CAT TTC ACA GCT GGG	870
V F N L T L S T E E I S N H F V Q N S Q	266
GTT TTC AAT CTC ACT CTC TCC ACC GAA GAG ATT TCC AAC CAT TTT GTT CAA AAC TCT CAA	930
G L G N V L S R I A E I Y I L S Q P F M	286
GGC CTT GGC AAC GTG CTC TCC CGG ATT GCA GAG ATC TAC ATC TTG TCC CAG CCC TTC ATG	990
V R I M A T E P P I I N L Q P G N F T L	306
GTG AGG ATC ATG GCC ACA GAG CCT CCC ATA ATC AAT CTA CAA CCA GGC AAT TTC ACC CTG	1050
D I P A S I M M L T Q P K N S T V E T I	326
GAC ATC CCT GCC TCC ATC ATG ATG CTC ACC CAA CCC AAG AAC TCC ACA GTT GAA ACC ATC	1110

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Fig. 5B

V	S	M	D	F	V	A	S	T	S	V	G	L	V	I	L	G	Q	R	L	346
GTT	TCC	ATG	GAC	TTC	GTT	GCT	AGT	ACC	AGT	GTT	GGC	CTG	GTT	ATT	TTG	GGA	CAA	AGA	CTG	1170
V	C	S	L	S	L	N	R	F	R	L	A	L	P	E	S	N	R	S	N	366
GTC	TGC	TCC	TTG	TCT	CTG	AAC	AGA	TTC	CGC	CTT	GCT	TTG	CCA	GAG	TCC	AAT	CGC	AGC	AAC	1230
I	E	V	L	R	F	E	N	I	L	S	S	I	L	H	F	G	V	L	P	386
ATT	GAG	GTC	TTG	AGG	TTT	GAA	AAT	ATT	CTA	TCG	TCC	ATT	CTT	CAC	TTT	GGA	GTC	CTC	CCA	1290
L	A	N	A	K	L	Q	Q	G	F	P	L	P	N	P	H	K	F	L	F	406
CTG	GCC	AAT	GCA	AAA	TTG	CAG	CAA	GGA	TTT	CCT	CTG	CCC	AAT	CCA	CAC	AAA	TTC	TTA	TTC	1350
V	N	S	D	I	E	V	L	E	G	F	L	L	I	S	T	D	L	K	Y	426
GTC	AAT	TCA	GAT	ATT	GAA	GTT	CTT	GAG	GGT	TTC	CTT	TTG	ATT	TCC	ACC	GAC	CTG	AAG	TAT	1410
E	T	S	S	K	Q	Q	P	S	F	H	V	W	E	G	L	N	L	I	S	446
GAA	ACA	TCC	TCA	AAG	CAG	CAG	CCA	AGT	TTC	CAC	GTA	TGG	GAA	GGT	CTG	AAC	CTG	ATA	AGC	1470
R	Q	W	R	G	K	S	A	P	*											456
AGA	CAG	TGG	AGG	GGG	AAG	TCA	GCC	CCT	TGA											1500
TTGCCGGTTTGCAATTCA	CCCCCAGGAAGTAAATGGTCCCTTAATCCTACA	ACTACTGTAAACCCAGAAAGGAAAGACAGT	1579																	
ACACACTGGAATTGTAAAGCCCTTGTGAATTGCTTAGGCAGAAAGTTTCTTTCTTAAGCCCTTCAGGAACCCAGAAATAA	1658																			
GGCAGACTCTGTAAAGGGATAAATAGAGGTGTCTGAATGTGAGTGATGCATGCTGCGTGTCTGTGTTATGTTG	1737																			
TTTGTTTGTGGGCAAGAAAGATTCTAGGACAAGAGCTAGGCATGTACTTCTGACCAGGTGGGTAAGCAACTCTAAG	1816																			

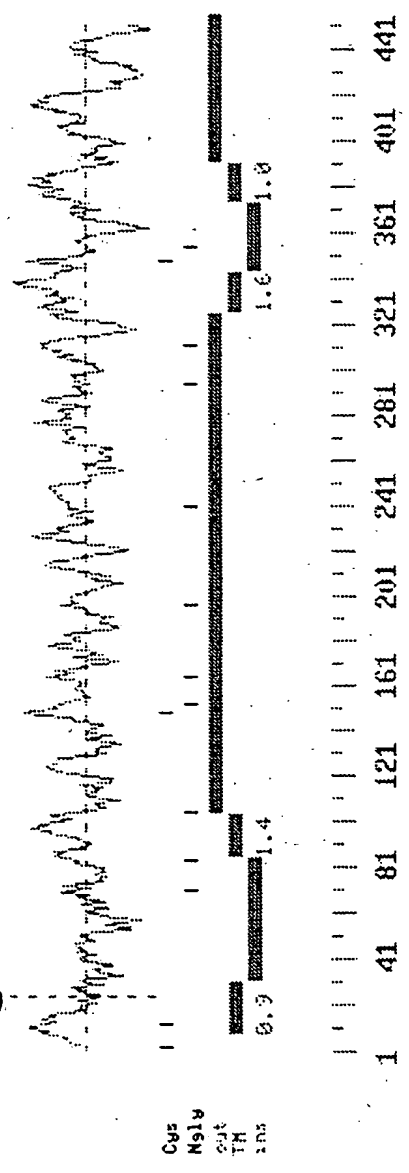
Fig. 5C

TCTGTATTGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTTCCTCCCTACCTGCATATTGGTTTC 1895  
ATGTTTATATTCACTGTTACTATCTTCTGTGTTTAAATTGTTTCTATCAAAAAAAAAAAAAAAAAAAGGGC 1974  
GGCCGC 1980

**Fig. 5D**

004250" E9084560

Fig. 5E



```

10      20      30      40      50      60
286 MCTKT-IPVLWGCFL-LWNLYVSSQTIYPGIKARITQALDYGVAQGMKMIQMLKEKKLPDLGSESL
:      :      :      :      :      :      :      :      :      :      :
BPI MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNYNFSNIKISAFSPNTSLAFVPGVGIGKALTNHGTANISTDWGFESPLFVLYNSFAEPM--
:      :      :      :      :      :      :      :      :      :      :
BPI KIKHLGKGHYFYMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130

140      150      160      170      180      190      200
286 -----KPI-----LKN-LNEMLCPIIASE
:      :      :      :      :      :      :      :      :      :      :
BPI SISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140      150      160      170      180      190      200

160      170      180      190      200      210      220
286 VKA-LNANLSTLEVLTKIDNYTLLDYSLISSPEITENYLDNLKGVFYPLENLTDPFPFVFLPERSN
:      :      :      :      :      :      :      :      :      :      :
BPI VSSKLQPYFQTLPVMTKIDSVAGINYLVAAPPATTAETLDVQMKGEFFYSENHHNPPPFAPPVMEFPAHD
210      220      230      240      250      260      270

```

Fig. 5F

09780360 : 057100

	230	240	250	260	270	280	290
2286	SMLYIGIAEYFFKSASFAHFTAGVFNLTLSLEEISNH--FVQNSQGLGNVLRSIAEIYILSQPFMVRIMA						
	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :						
BBPI	RMVYLGLSDYFFNTAGLVYQEAGVLKMTLRRDDMI PKESKFRLTTKKFGTFLPEVAKKFP-NMKIQIHVSA						
	280	290	300	310	320	330	340

	300	310	320	330	340	350	360
286	TEPPIINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTVGLVILGQRLVCSLSLNRFRALPE						
	. : : : : . : : . . . : : : : . . . : : : : . : : : . : : . : . : . : . : . : . : .						
BBPI	STPPHLSVQPTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRVLVGELKLDRLLELKH						
	350	360	370	380	390	400	410

	370	380	390	400	410	420	430
2286	SNRSNIEVLRFFENILSSILHFGVLPLANAKLQGFPLPNPHKFLFVNSDIEVLEGEFLLISTDLKYETSSK						
	:: :: :	:: :: :	:: :: :	:: :: :	:: :: :	:: :: :	:
BBPI	SNIGFPVELLDIMNYIVPILVLP RVNEKLQKGFP LPTPARVOLYNVVLP HQNFLLFGADVYK----						
	420	430	440	450	460	470	480

286 QQPSEHVWEGNLI SRQWRGKSAP 440 450

-----BPI

5G  
Firm



```

10      20      30      40      50      60
286 MCTKTIPVLWGCFLWNLYVSSSQTI--YPGIKARITQRALDYGQAGMKMIEQMLKEKKLPDLSGSESL
: . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP MGALARAL--PSILLALLTSTPEALGANPGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTG--DL
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNYNFSNIKISAFSPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPM--
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP RIPHVGRGRYEFHSLNIHEFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130

286 -----KPI-----140     150
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP SISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVKGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140     150     160     170     180     190     200

160     170     180     190     200     210     220
286 VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDNLKGVFYPLENLTDPFSPVPFVLPERSN
: . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP VSSKLQPYFQTLPMVTKIDSVAGINYGLVAPPATTAETLDVQMKGEFYSENHHNPPFPFAPVMEFFAAHD
210     220     230     240     250     260     270

```

Fig. 5H

09578063 052400

[illegible]

```

300      310      320      330      340      350      360
286 TEPIINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTVGLVILGQRLVCSLSLNRFRALPE
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
REN P STPPHLSVQPTGLTFYPAVDVQALAVLPNSSLASLFLIGMHTTGSMEVSAESNRVLVGELKLDRLLELKH
350      360      370      380      390      400      410

```

```

      370      380      390      400      410      420      430
286 SNRSNIEVLFENILSSILHFGVLPLANAKLQQGFPLPNPHKFLFVNSDIEVLEGLLISTDCLKYETSSK
      :: . : . . . . . :: . . . . . : . . . . . :
RENPF SNIGFFVELLDIMNYIVPILVLRVNEKLQKGFP LPTPARVQLYNVLQPHQNFLFGADVVK-----
      420      430      440      450      460      470      480

```

286 QPSPFHVWEGNLSROWRGKSAP

RENP-----

Fi. 51

GTCGACCCACGCGTCCGGGAATTGCAGCAGGAAATATGTGAAGAGTTTTTAAACCCACAAATCTTCTTACTTTAGA	79
M L E T L S R Q	
ATTAGTTGTACATTGGCAGGAAAAATAAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG	8 149
W I V S H R M E M W L L I L V A Y M F Q	28
TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG	209
R N V N S V H M P T K A V D P E A F M N	48
AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT	269
I S E I I Q H Q G Y P C E E Y E V A T E	68
ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA	329
D G Y I L S V N R I P R G L V Q P K K T	88
GAT GGG TAT ATC CTT TCT GTT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA	389
G S R P V V L L Q H G L V G G A S N W I	108
GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT	449
S N L P N N S L G F I L A D A G F D V W	128
TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG	509
M G N S R G N A W S R K H K T L S I D Q	148
ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA	569

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Fig. 6A

D	E	F	W	A	F	S	Y	D	E	M	A	R	F	D	L	P	A	V	I	168	
GAT	GAG	TTC	TGG	GCT	TTC	AGT	TAT	GAT	GAG	ATG	GCT	AGG	TTT	GAC	CTT	CCT	GCA	GTG	ATA	629	
N	F	I	L	Q	K	T	G	Q	E	K	I	Y	Y	V	G	Y	S	Q	G	188	
AAC	TTT	ATT	TTG	CAG	AAA	ACG	GGC	CAG	GAA	AAG	ATC	TAT	TAT	GTC	GGC	TAT	TCA	CAG	GGC	689	
T	T	M	G	F	I	A	F	S	T	M	P	E	L	A	Q	K	I	K	M	208	
ACC	ACC	ATG	GGC	TTT	ATT	GCA	TTT	TCC	ACC	ATG	CCA	GAG	CTG	GCT	CAG	AAA	ATC	AAA	ATG	749	
Y	F	A	L	A	P	I	A	T	V	K	H	A	K	S	P	G	T	K	F	228	
TAT	TTT	GCT	TTA	GCA	CCC	ATA	GCC	ACT	GTT	AAG	CAT	GCA	AAA	AGC	CCC	GGG	ACC	AAA	TTT	809	
L	L	L	P	D	M	I	K	I	K	G	L	F	G	K	K	E	F	L	Y	Q	248
TTG	TTG	CTG	CCA	GAT	ATG	ATG	ATC	AAG	GGA	TTG	TTT	GGC	AAA	AAA	GAA	TTT	CTG	TAT	CAG	869	
T	R	F	L	R	Q	L	V	I	Y	L	C	G	Q	V	I	L	D	Q	I	268	
ACC	AGA	TTT	CTC	AGA	CAA	CTT	GTT	ATT	TAC	CTT	TGT	GGC	CAG	GTG	ATT	CTT	GAT	CAG	ATT	929	
C	S	N	I	M	L	L	L	G	G	F	N	T	N	N	M	N	M	S	R	288	
TGT	AGT	AAT	ATC	ATG	TTA	CTT	CTG	GGT	GGA	TTC	AAC	ACC	AAC	AAT	ATG	AAC	ATG	AGC	CGA	989	
A	S	V	Y	A	A	H	T	L	A	G	T	S	V	Q	N	I	L	H	W	308	
GCA	AGT	GTA	TAT	GCT	GCC	CAC	ACT	CTT	GCT	GGA	ACA	TCT	GTG	CAA	AAT	ATT	CTA	CAC	TGG	1049	
S	Q	A	V	N	S	G	E	L	R	A	F	D	W	G	S	E	T	K	N	328	
AGC	CAG	GCA	GTG	AAT	TCT	GGT	GAA	CTC	CGG	GCA	TTT	GAC	TGG	GGG	AGT	GAG	ACC	AAA	AAT	1109	

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Fig. 6B

L	E	K	C	N	Q	P	T	P	V	R	Y	R	V	R	D	M	T	V	P	348
CTG	GAA	AAA	TGC	AAT	CAG	CCA	ACT	CCT	GTA	AGG	TAC	AGA	GTC	AGA	GAT	ATG	ACG	GTC	CCT	1169
T	A	M	W	T	G	G	Q	D	W	L	S	N	P	E	D	V	K	M	L	368
ACA	GCA	ATG	TGG	ACA	GGA	GGT	CAG	GAC	TGG	CTT	TCA	AAT	CCA	GAA	GAC	GTG	AAA	ATG	CTG	1229
L	S	E	V	T	N	L	I	Y	H	K	N	I	P	E	W	A	H	V	D	388
CTC	TCT	GAG	GTG	ACC	AAC	CTC	ATC	TAC	CAT	AAG	AAT	ATT	CCT	GAA	TGG	GCT	CAC	GTG	GAT	1289
F	I	W	G	L	D	A	P	H	R	M	Y	N	E	I	I	H	L	M	Q	408
TTC	ATC	TGG	GGT	TTG	GAT	GCT	CCT	CAC	CGT	ATG	TAC	AAT	GAA	ATC	ATC	CAT	CTG	ATG	CAG	1349
Q	E	E	T	N	L	S	Q	G	R	C	E	A	V	L	*					424
CAG	GAG	GAG	ACC	AAC	CTT	TCC	CAG	GGA	CGG	TGT	GAG	GCC	GTA	TTG	TGA					1397
AGCATCTGACACTGACGATCTTAGGACAACCTCCTGAGGGATGGGGCTAGGACCCCATGAAGGCAGAAATTACGGAGAGCA	1476																			
GAGACCTAGTATACATTTTTCAGATTCCCTGCACCTGGCACAATAATCCGACACTTACATTTTCTGTAAA	1555																			
TTAAAGTACTTATTAGGTAATAAGAGGTTTGTATGCTATTATATATCTCTTAAACACACCTATGTTTTCTATAAGCCAT	1634																			
AGCCAGAAAATATCTAGACATTCTCTATATCATTCAGGTAAATCTCTTAAACACACCTATGTTTTCTATAAGCCAT	1713																			
ATTTTGGAGCACTAAAGTAAATGGCAAAATGGGACAGATATTGAGGCTGGAGTCTGTGGATTATTGTGACTTTGA	1792																			
CAAAATAAGCTAGACATTTTCACCTTGTGTCACAGACACATAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA	1871																			
CAACAACAAAATCAGTGTTACAGTATGGATGAAATCTATGTTAAGCATTTCTCAGAATAAGGCCAAGTTTATAGTTGCA	1950																			
TCTCAGGGAAGAAAATTTTATAGGATGTTTATGAGTTCTCCAATAAATGCATTCTGCATTACATAAAAAAAAAAAAA	2029																			
AAAAAGGGCGCGCGC	2044																			

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Fig. 6C

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10      20      30      40      50      60      70
294 MLETLRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTKAVDPEAFMNISEIIHQHGYPCEEYEVATEDG
:      :      :      :      :      :      :
HLP M-----WLL---LTMASLISVLGTTGHLFGKLH---PGSPEVTMNISOMITYWGYPNEEYEVVTEDEG
10      20      30      40      50

80      90      100     110     120     130     140
294 YILSVNRIPRGLVQPKKTGSRPVPVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNWSRK
:      :      :      :      :      :      :
HLP YILEVNRIPYGKKNSGNTGQRPVFLQHGLLASATNWIISNLPNNSLAFILADAGYDVWLGNRGNTWARR
60      70      80      90      100     110     120

150     160     170     180     190     200     210
294 HKTLSDQDEFWAFSYDEMAREFDLPVINFILQKTGQEKIYYVGYSGTTMGFIAFSTMPELAQKIKMYF
:      :      :      :      :      :      :
HLP NLYYSPDSVEFWAFSFDEMAKYDLPATIDFIVKKTGQQLHYVGHSGQTTIGFIAFSTNPSLAKRIKTFY
130     140     150     160     170     180     190

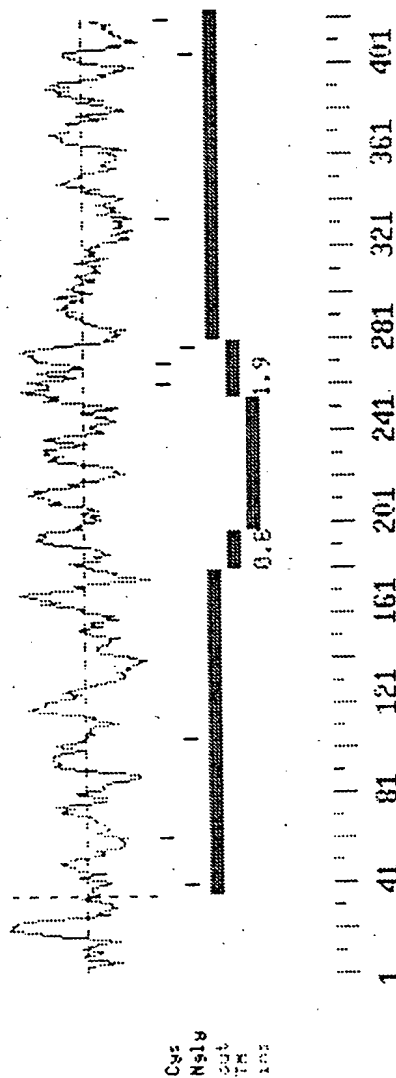
220     230     240     250     260     270
294 ALAPIATVKHAKSPGTFKFLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGQVILDQICSNIMLLLGGF
:      :      :      :      :      :      :
HLP ALAPVATVKYTKSLINKLRFPQSLFKFIFGDKIF-YPHNFFDQFLATEVCSREMLNLLCSNALFIICGF
200     210     220     230     240     250     260

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Fig. 6D



Fig. 6F







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280      290      300      310      320      330      340
294 FNTNNMMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVP
    :: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL FNERNLNMSRVDVYTTHTSPAGTSVQNMLHWSQAVKFKQAFDQWSSAKNYFHYNQSYPTYNVKDMLVP
270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNIEIHLMQQEEETNLSQGR
    :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL TAVWSGGHDWLADVVDVNILLTQITNLVFHESIPWEHLDFIWGLDAPWRLYNKIINLMRKYQ-----
340      350      360      370      380      390

420
294 CEAVL

LAL -----

```

Fig. 6H

GTCGACCCACGGCTCCACGGGAGGGCTCCCGGGGCGAGCATTTGCCCCCTGCACCACCTCACCAAG ATG GCT	75
T L G H T F P F Y A G P K P T F P M D T	22
ACT TTG GGA CAC ACA TTC CCC TTC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC	135
T L A S I I M I F L T A L A T F I V I L	42
ACT TTG GCC AGC ATC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC GTC ATC CTG	195
P G I R G K T R L F W L L R V V T S L F	62
CCT GGC ATT CGG GGA AAG ACG AGG CTG TTC TGG CTG CTT CGG GTG GTG ACC AGC TTA TTC	255
I G A A I L A V N F S S E W S V G Q V S	82
ATC GGG GCT GCA ATC CTG GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC	315
T N T S Y K A F S S E W I S A D I G L Q	102
ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG	375
V G L G G V N I T L T G T P V Q Q L N E	122
GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACA GGG ACC CCC GTG CAG CAG CTG AAT GAG	435
T I N Y N E E F T W R L G E N Y A E E C	142
ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT	495
A K A L E K G L P D P V L Y L A E K F T	162
GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT	555

Fig. 7A

P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	CGC	CAG	TAC	CGC	CTG	CGG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CTC	ACC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795
L	H	T	H	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	CTG	TGT	GTG	855
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095

Fig. 7B

L \* 344  
TTA TAA 1101

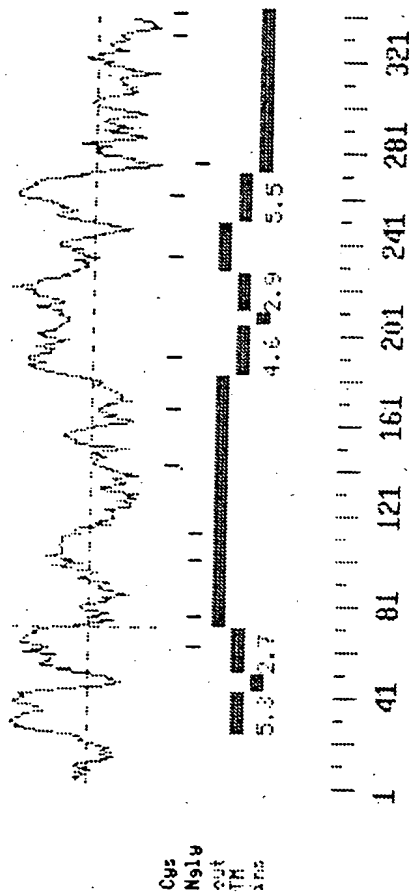
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TGGAGTCGACGCAGAGAATCAGGTTTCACAGCACTGCGGAGAGTGTACTAGGCTGTCTCCAGCCCGAGCGAAGCTCATGA 2049  
GGACGTGCGACCCCGCGGAGAGCCATGAAAATTAAATGGGAAACACAGTTTTTAAAAAAGGGCGG 2128  
GCGGC 2133

Fig. 7C

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Fig. 7D



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10      20      30      40      50      60      70
296 MATLGHTFFYAGPKPTFPMDDTLASIIIMIFLTALATFIVILPGIRKTRFLWLLRVVTSLFIGAAILAV
:  . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
CRP M-RIAH-----ASSRGNI-----SIFSVELIPLIAYILILPGVR-RKRVVTTVTYVLMMLAVGGALIAS
10      20      30      40      50

296 NFSSEWSVGQVSTNTSYKAFSSEWISADIGLQVGLGGVNITL-----TGTPVQQLNETIN--YNEEFTW
. . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
CRP LIYPCWASGSQMIYTQFRGHSNERILAKIGVEIGLQKVNVTCLKFERLLSSNDVLPGSDMTELYNEGEDFI
60      70      80      90      100      110      120

296 RLGENYAECAKALEKGLDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAFLCWLLANV-MLSM
. . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
CRP SGISSMAEALHHGLENGLPYPMLSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCCLSVVLMFL
130     140     150     160     170     180     190

296 PVLVYGGYMLLATGIFQLLALLFFSMATSLTSPCPLHL---GASVLTHHGPAP----WITLTGLLCVL
:  . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . :
CRP PHNAYKS--ILATGISCLIACLVYL---LLSPCELRIAFTGENFERVDLTATFSFCFYLI FAIGILCVL
200     210     220     230     240     250     260

```

Fig. 7E

270	280	290	300	310	320
296	LGLAMAVAH	RMQPHRLK	AFFNQSV	DEDPMLEW	-----SPEEGLLSPRY--RSMADSPKSQDIPLSEAS
	:::...	:::...	:::...	:::...	:::...
CRP	CGLGLGICE	HWRIYTL	STFLDAS	LDLDEHVG	PKWKKLPTGGPALQGVQIGAYGTNTTNSRRDKNDISSDKTA
	270	280	290	300	310 320 330
330	296	STKAY	-----CK	-----E	AHPKDPD-----CA---L
	..	..	::	...	::
CRP	GSSGFQSR	TSTCQSS	ASSASLRS	QSSIE	TVHDEAELE
	340	350	360	370	380
					THVHFLQEP

Fig. 7F